

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36

RESULT 2

US-08-896-501A-1
Sequence 1, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment

US-08-896-501A-1

Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36

RESULT 3

US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIABDDENLESD 36

RESULT 4

US-08-896-501A-2
Sequence 2, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

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OM protein - protein search, using SW model

Run on: May 13, 2005, 12:17:10 ; Search time 42 Seconds
(without alignments)
63.985 Million cell updates/sec

Title: US-09-711-896A-1

Perfect score: 188
Sequence: 1 MAAPVEDNCIFVAMKPTDNLTYIAEDDENLSD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	188	100.0	41 2	US-08-896-501A-1 Sequence 1, Appl
3	188	100.0	193 2	US-08-896-605A-2 Sequence 2, Appl
4	188	100.0	193 3	US-08-896-501A-2 Sequence 2, Appl
5	188	100.0	193 3	US-08-832-180-9 Sequence 4, Appl
6	188	100.0	193 4	US-10-105-080-4 Sequence 6, Appl
7	188	100.0	193 4	US-09-949-016-6095 Sequence 6095, Ap
8	179	95.2	193 4	US-09-597-576-2 Sequence 2, Appl
9	139.5	74.2	133 4	US-09-817-265A-2 Sequence 2, Appl
10	139.5	74.2	193 4	US-09-917-265A-8 Sequence 8, Appl
11	132	70.2	193 4	US-09-445-724B-2 Sequence 2, Appl
12	132	70.2	193 4	US-09-445-724B-6 Sequence 6, Appl
13	110	58.5	192 4	US-10-105-080-5 Sequence 318, App
14	50	26.6	78 4	US-09-749-637A-318 Sequence 13, Appl
15	50	26.6	536 4	US-08-653-648A-13 Sequence 13, Appl
16	50	26.6	536 4	US-09-564-418-9 Sequence 6689, Ap
17	49.5	26.3	78 4	US-09-107-532A-6689 Sequence 6689, Ap
18	49	26.1	367 4	US-09-248-796A-27329 Sequence 6071, Ap
19	49	26.1	367 4	US-09-134-000C-6071 Sequence 16, Appl
20	49	26.1	747 3	US-08-089-397A-15 Sequence 17, Appl
21	49	26.1	776 1	US-07-603-133B-17 Sequence 20, Appl
22	49	26.1	776 1	US-07-603-133B-20 Sequence 15, Appl
23	49	26.1	776 1	US-08-089-397A-15 Sequence 2, Appl
24	48.5	25.8	464 1	US-07-991-867B-2 Sequence 2, Appl
25	48.5	25.8	464 1	US-08-107-755A-2 Sequence 2, Appl
26	48.5	25.8	464 2	US-08-544-332-2 Sequence 2, Appl
27	48.5	25.8	464 4	US-09-370-861A-2 Sequence 2, Appl

28	48	25.5	93 4	US-09-134-000C-6731 Sequence 6731, Ap
29	48	25.5	520 4	US-09-248-796A-20803 Sequence 20803, A
30	48	25.5	688 3	US-09-113-790A-3 Sequence 3, Appl
31	47.5	25.3	1039 4	US-09-328-352-5474 Sequence 5474, Ap
32	47.5	25.3	1806 4	US-09-919-497-56 Sequence 56, Appl
33	47	25.0	475 3	US-09-212-247C-4 Sequence 4, Appl
34	47	25.0	514 4	US-09-746-359A-39 Sequence 39, Appl
35	47	25.0	546 4	US-09-746-359A-37 Sequence 37, Appl
36	47	25.0	694 2	US-08-895-522-4 Sequence 4, Appl
37	47	25.0	694 3	US-09-195-391-4 Sequence 15, Appl
38	47	25.0	775 1	US-07-603-133B-15 Sequence 16, Appl
39	47	25.0	775 1	US-07-603-133B-16 Sequence 323, App
40	46.5	24.7	818 4	US-09-538-092-323 Sequence 14464, A
41	46	24.5	155 4	US-09-248-796A-14464 Sequence 34881, A
42	46	24.5	166 4	US-09-270-767-34881 Sequence 34098, A
43	46	24.5	166 4	US-09-270-767-50098 Sequence 42900, A
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45	46	24.5	266 3	US-09-414-276-8

ALIGNMENTS

RESULT 1
US-08-896-605A-1
Sequence 1, Application US/08896605A
Patent No. 5879942
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment
US-08-896-605A-1
Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT "African swine fever virus encodes a CD2 homolog responsible for the
 RT adhesion of erythrocytes to infected cells.";
 RL J. Virol. 67:5312-5320(1993).
 RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93277388; PubMed=8503790;
 RA Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
 RT "Structure and expression in E. coli of the gene coding for protein
 RL p10 of African swine fever virus.";
 RN Arch. Virol. 130:93-107(1993).
 RP [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94065656; PubMed=8245848;
 RA Alcantar A., Angulo A., Vinuela E.;
 RT "Mapping and sequence of the gene encoding the African swine fever
 RL virion protein of M(2) 11500.";
 RN J. Gen. Virol. 74:2317-2324(1993).
 RP [20]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94133966; PubMed=8293992; DOI=10.1016/0378-1119(93)90453-A;
 RA Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
 RT "The DNA polymerase-encoding gene of African swine fever virus:
 RL sequence and transcriptional mapping.";
 RN Gene 136:103-110(1993).
 RP [21]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94187118; PubMed=8139051;
 RA Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
 RL Vinuela E.;
 RT "Multigene families in African swine fever virus: family 505.";
 RN J. Virol. 68:2746-2751(1994).
 RP [22]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94233765; PubMed=8178480;
 RA De la Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.;
 RT "Nucleotide sequence and variability of the inverted terminal
 RL repetitions of African swine fever virus DNA.";
 RN Virol. 201:152-156(1994).
 RP [23]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=91820291; PubMed=11831707;
 RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
 RT "Analysis of the complete nucleotide sequence of African swine fever
 RL virus.";
 RN Virol. 208:249-278(1995).
 RP [24]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 QY Query Match 28.5%; Score 53.5; DB 2; Length 1055;
 DB Best Local Similarity 27.3%; Pred. No. 1.5e+02;
 Matches 12; Conservative 8; Mismatches 15; Indels 9; Gaps 1;

GN Name=dapE;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteriaceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RX MEDLINE=95331541; PubMed=7607469; DOI=10.1016/0378-1119(94)00668-I;
 RA Vitor J.M., Morgan R.D.;
 RT "Two novel restriction endonucleases from Campylobacter jejuni.";
 RL Gene 157:109-110(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RA Vitor J.M.B.;
 RT "Restriction and modification systems in Campylobacter jejuni and C.
 RL coli.";
 RN Theiss (1999), University of Lisbon, Lisbon, Portugal.
 RP [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RA Vitor J.M.B.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF264911; AAF77191.1; -;
 DR InterPro: IPR001261; ARGE dapE.
 DR PROSITE: PS00758; ARGE_DAPF_CpG2_1; UNKNOWN_1.
 FT NON TER 70 70
 SQ SEQUENCE 70 AA; 7900 MW; 89A614EDCD9DCE45 CRC64;
 QY Query Match 28.2%; Score 53; DB 2; Length 70;
 DB Best Local Similarity 36.0%; Pred. No. 7.6;
 Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 ID 5 PVEDNCINPVAMKFDINTLYFAED 29
 DB 17 PNDGALNFIAMELSDFAEFIEKE 41
 QY Query Match 28.2%; Score 53; DB 2; Length 99;
 DB Best Local Similarity 47.6%; Pred. No. 11;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 ID 4 EPVEDNCINPVAMKFDINTLY 24
 DB 79 ETLRDNAIFVARKOLENKVY 99
 Search completed: May 13, 2005, 12:25:11
 Job time : 177 secs

065146 ID 065146 PRELIMINARY; PRT; 1055 AA.
 AC 065146;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Helicase.
 GN Name=PI055L;
 OS African swine fever virus (ASFV).
 OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
 OK NCBI_TaxID=10497;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90223993; PubMed=2327074;
 RA Lopez-Otin C., Freije J.M.P., Parra F., Mendez E., Vinnela E.;
 RT "Mapping and sequence of the gene coding for protein p72, the major
 RL capsid protein of African swine fever virus."; Virol. 175:477-484(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90357780; PubMed=2389555;
 RA Blasco R., Lopez-Otin C., Munoz M., Bockamp E.-O., Simon-Mateo C.,
 RA Vinnela E.;
 RT "Sequence and evolutionary relationships of African swine fever virus
 RL thymidine kinase."; Virol. 178:301-304(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90219204; PubMed=2325202;
 RA Alendral J.M., Almazan F., Blasco R., Vinnela E.;
 RT "Multigene families in African swine fever virus: family 110."; Virol. 64:2064-2072(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90219205; PubMed=2325203;
 RA Gonzalez A., Cayo V., Almazan F., Alendral J.M., Ramirez J.C.,
 RA De La Vega I., Blasco R., Vinnela E.;
 RT "Multigene families in African swine fever virus: family 360."; Virol. 64:2073-2081(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=91134988; PubMed=1994575;
 RA Camacho A., Vinnela E.;
 RT "Protein p22 of African swine fever virus: an early structural protein
 RL that is incorporated into the membrane of infected cells."; Virol. 181:251-257(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92087485; PubMed=1309282;
 RA Rodriguez J.M., Salas M.L., Vinnela E.;
 RT "Genes homologous to ubiquitin-conjugating proteins and eukaryotic
 RL transcription factor SII in African swine fever virus."; Virol. 186:40-52(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93174976; PubMed=8438592;
 RA Yanez R.J., Vinnela E.;
 RT "African swine fever virus encodes a DNA ligase."; Virol. 193:531-536(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92263807; PubMed=1316688;
 RA Garcia-Beato R., Freije J.M.P., Lopez-Otin C., Blasco R., Vinnela E.,
 RA Salas M.L.;
 RT "A gene homologous to topoisomerase II in African swine fever virus.";

RL Virol. 188:938-947(1992).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92260660; PubMed=1583732;
 RA Alcant A., Angulo A., Lopez-Otin C., Munoz M., Freije J.M.P.,
 RA Carrascosa A.L., Vinnela E.;
 RT "Amino acid sequence and structural properties of protein p12, an
 RL African swine fever virus attachment protein."; Virol. 66:3860-3868(1992).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94091056; PubMed=8266720; DOI=10.1016/0168-1702(93)90016-G;
 RA Freije J.M., Lain S., Vinnela E., Lopez-Otin C.;
 RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
 RL gene from African swine fever virus."; Virus Res. 30:63-72(1993).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93346971; PubMed=8393914;
 RA Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinnela E.;
 RT "African swine fever virus thymidylate kinase gene: sequence and
 RL transcriptional mapping."; J. Gen. Virol. 74:1633-1638(1993).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93281390; PubMed=8506138;
 RA Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinnela E.;
 RT "African swine fever virus encodes two genes which share significant
 RL homology with the two largest subunits of DNA-dependent RNA
 RN polymerases."; Nucleic Acids Res. 21:2423-2427(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93174941; PubMed=8382399;
 RA Pena L., Yanez R.J., Revilla Y., Vinnela E., Salas M.L.;
 RT "African swine fever virus guanylyltransferase."; Virol. 193:319-328(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93327788; PubMed=8335009;
 RA Simon-Mateo C., Andres G., Vinnela E.;
 RT "Polyprotein processing in African swine fever virus: a novel gene
 RL expression strategy for a DNA virus."; EMBO J. 12:2977-2987(1993).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93233210; PubMed=8474154;
 RA Prados F.J., Vinnela E., Alcant A.;
 RT "Sequence and characterization of the major early phosphoprotein p32
 RL of African swine fever virus."; J. Virol. 67:2475-2485(1993).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94085774; PubMed=8262374; DOI=10.1016/0378-1119(93)90090-P;
 RA Yanez R.J., Rodriguez J.M., Boursnell M.E.G., Rodriguez J.F.,
 RA Vinnela E.;
 RT "Two putative African swine fever virus helicases similar to yeast
 RL 'DnaH' pre-mRNA processing proteins and vaccinia virus ATPases D1L
 and D6R."; Gene 134:161-174(1993).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93353606; PubMed=8102411;
 RA Yanez R.J., Almazan F., Vinnela E., Rodriguez J.F.;

QY 5 PVED-----NCINPAMKPIDNTLYPIA-EDDENTLE 34
 DB 161 PVEDVNCIFOGNCPRFISCEPAHNNNSWYTFESDEDAQ 199

RESULT 35

Q96410 PRELIMINARY; PRT; 417 AA.
 AC 096410, 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Serum response factor.
 GN Name=SRF;
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
 CC Hydridae; Hydra.
 RX NCBI_TaxId=6087;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21369530; PubMed=11476573; DOI=10.1006/dbio.2001.0335;
 RA Hoffmann U, Krolner M;
 RT "A possible role for the chidarian homologue of serum response factor
 in decision making by undifferentiated cells."
 RL Dev. Biol. 236:304-315 (2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL, AF306544; AAK81817.1; -.
 DR HSPF, F11831; 1HEX.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PR00319; SRF-TF; 1
 DR PRINTS; PR00404; MADSBOXMIN.
 DR SMART; SM00432; MADS_BOX_1; 1.
 DR PROSITE; PS00350; MADS_BOX_2; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 417 AA; 47097 MW; 4B916B815605515 CRC64;

Query Match 28.7%; Score 54; DB 2; Length 417;
 Best Local Similarity 35.5%; Pred. No. 43;
 Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 6 VEDNCINPAMKPIDNTLYPIAEDDENTLESD 36
 DB 42 VEDTHLSFVQPLIVDTKHYOSLDEDLTD 72

RESULT 36

Q7Y256 PRELIMINARY; PRT; 921 AA.
 AC 07Y256, 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Ubiquitin-specific protease, probable.
 GN ORFNames=UMB.672;
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 CC Cryptosporidiidae; Cryptosporidium.
 RX NCBI_TaxId=5807;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bankler A.T., Spriggs H.F., Partmann B., Konfortov B.A., Madera M.,
 RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 Cryptosporidium parvum."
 RL Genome Res. 0:0-0(2003).
 DR EMBL; BX538553; CAD98271.1; -.
 DR GO; GO:0004197; P:cysteine-type endopeptidase activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro; IPR001394; Peptidase_C19.
 DR InterPro; IPR004449; UBA.
 DR InterPro; IPR001607; Znf_UBP.
 DR Pfam; PF00443; UCH; 1.
 DR Pfam; PF02148; Zf-UBP; 1.
 DR SMART; SM0165; UBA; 1.
 DR PROSITE; PS50030; UBA; 1.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS02353; UCH_2_3; 1.
 DR Protease.
 KW SEQUENCE 921 AA; 104507 MW; 9447C853FF572F67 CRC64;

Query Match 28.7%; Score 54; DB 2; Length 921;
 Best Local Similarity 33.3%; Pred. No. 1,1e+02;
 Matches 9; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 4 BEVEDNCINPAMKPIDNTLYPIAEDD 30
 DB 879 QPTBSCSSSIWRNDIKYLSKEDD 905

RESULT 37

Q86A22 PRELIMINARY; PRT; 494 AA.
 AC 086A22, 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Similar to Gallus gallus (Chicken). Cytochrome P-450.
 OS Dictyostelium discoideum (slime mold).
 CC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 RX NCBI_TaxId=44689;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092822; PubMed=12097910; DOI=10.1038/nature00847;
 RA Glockner G., Richinger L., Szafrenki K., Pachter J., Dear P.,
 RA Lehmann R., Baumgart C., Patra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
 RL Nature 418:79-85(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL, AC117175; AA052115.1; -.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002401; EP450I.
 DR Pfam; PR00067; P450; 1.
 DR PRINTS; PR00463; EP450I.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Heme; Monooxygenase; Oxidoreductase.
 KW SEQUENCE 494 AA; 57571 MW; 26B8CA28F2ED2486B CRC64;

Query Match 28.5%; Score 53.5; DB 2; Length 494;
 Best Local Similarity 44.0%; Pred. No. 62;
 Matches 11; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 8 DNCINPAMKPIDNTLYPIAEDDEN 32
 DB 248 NNCNPF-QPLIDNLIKNSIDDDDD 271

RESULT 38

RC STRAIN-S288C / AB972;
 RX MEDLINE-9524563; PubMed-7731988;
 RA Bussey H., Kadack D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Quellerette B.F.P., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RT "The nucleotide sequence of chromosome I from *Saccharomyces*
 RT *cerevisiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -1- FUNCTION: Involved in the transfer of acetyl-CoA into
 CC mitochondria. May also be involved in the metabolism of acetate
 CC and of ethanol.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + carnitine = CoA + O-
 CC acetylcarbitine.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane; outer side.
 CC -1- INDUCTION: By ethanol and by acetate. Repressed by glucose, and to
 CC a lesser extent, by galactose. Derepressed by glycerol.
 CC -1- SIMILARITY: Belongs to the carnitine/choline acetyltransferase
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X74553; CAA52647.1; -;
 DR EMBL: L28920; AAC09495.1; -;
 DR PIR: S53485; S53485.
 DR HSPSP: P47934; INDP.
 DR Germonline: J38421; -;
 DR SGD: S000000080; YAT1.
 DR GO: GO:0005739; C:mitochondrion; IDA.
 DR GO: GO:0006066; P:alcohol metabolism; IGI.
 DR GO: GO:0009437; P:carnitine metabolism; IMP.
 DR InterPro: IPR000542; Carn_acyl_trans.
 DR Pfam: PF00755; Carn_acyltransferase; 1.
 DR PROSITE: PS00439; ACYLTRANSF_C_1; FALSE_NEG.
 DR PROSITE: PS00440; ACYLTRANSF_C_2; 1.
 DR Kegg: K00000; Fatty acid metabolism; Mitochondrion; Transferase;
 KM Transport.
 FT ACT SITE 346 346 Potential.
 FT CONFLICT 25 25 T -> P (in Ref. 2).
 FT CONFLICT 393 393 Missing (in Ref. 2).
 FT CONFLICT 596 597 AS -> SF (in Ref. 2).
 FT CONFLICT 654 654 T -> A (in Ref. 2).
 FT CONFLICT 661 661 A -> T (in Ref. 2).
 SO SEQUENCE 688 AA; 77780 MW; 6445A08B59A5F64B CRC64;
 Query Match 29.3%; Score 55; DB 1; Length 688;
 Best Local Similarity 34.5%; Pred. No. 55;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 QY 8 DNCINPFAVKFIDNTLYFIADNLESD 36
 DB 260 DDCTWNRNKLIDSLFVCLDVAFAAD 288
 RESULT 33
 ID 06CUT7 PRELIMINARY; PRT; 862 AA.
 AC 06CUT7;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similar to *ca*|CA1657|IPF16022 *Candida albicans* unknown function.
 GN ORName=TLA0F160389;
 OS *Kluyveromyces fragilis* NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; *Kluyveromyces*.
 OX NCBI_TaxID=284550;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevers;
 RA Dutton B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Gottard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckrich J.M., Beyne E., Bleykasten C.,
 RA Bolerame A., Boyer J., Catterico L., Confiantieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hartave F., Henneguin C., Janniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaitre M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 WD repeats.
 DR EMBL: CR382126; CAG98510.1; -;
 DR InterPro: IPR001680; WD40.
 DR InterPro: IPR011046; WD40_like.
 DR Pfam: PF00400; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR Repeat; WD repeat.
 KW SEQUENCE 862 AA; 96845 MW; BP08B7AA74E1909 CRC64;
 Query Match 29.3%; Score 55; DB 2; Length 862;
 Best Local Similarity 42.3%; Pred. No. 71;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 4 EPVEDNCINPFAVKFIDNTLYFIAD 29
 DB 552 ETVADNKNIGNIQLEMCKNLYTSSD 577

RESULT 34
 ID 070SF7 PRELIMINARY; PRT; 439 AA.
 AC 070SF7;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE AGCP5851 (Fragment).
 GN Name=agc51593; ORName=ENSGANG00000011002;
 OS *Anopheles gambiae* str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; *Anopheles*.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB0100860; EA11778.1; -;
 DR InterPro: IPR006630; Lupus_La_dom.
 DR Pfam: PF05383; La; 1.
 FT NON_TER 1 1
 FT NON_TER 439 439
 SO SEQUENCE 439 AA; 45810 MW; 242AB05879D7B7ED CRC64;
 Query Match 29.0%; Score 54.5; DB 2; Length 439;
 Best Local Similarity 33.3%; Pred. No. 39;
 Matches 13; Conservative 7; Mismatches 10; Indels 9; Gaps 2;

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxId=158679;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshino A.,
 RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Sekimizu M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AF003135; BAB42852.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_ester.
 DR PRINTS; PRO011; ABHYDROLASE.
 KW Complete proteome.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;
 Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;
 Oy 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 Db 242 EPERDEVMRYI-LTFLNSVNTMGFIVEDEIVE 274
 RESULT 30
 ID 06G8G4 PRELIMINARY; PRT; 275 AA.
 AC 06G8G4
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN Ordered locus names=SA31689;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxId=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571857; CAG43492.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_ester.
 DR PRINTS; PRO011; ABHYDROLASE.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;
 Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;
 Oy 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 Db 242 EPERDEVMRYI-LTFLNSVNTMGFIVEDEIVE 274

Oy 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 Db 242 EPERDEVMRYI-LTFLNSVNTMGFIVEDEIVE 274
 RESULT 31
 ID 06GFT8 PRELIMINARY; PRT; 275 AA.
 AC 06GFT8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN Ordered locus names=SA1848;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxId=282458;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571856; CAG40839.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_ester.
 DR PRINTS; PRO011; ABHYDROLASE.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 275 AA; 31880 MW; 2358B0A22DA8ABE1 CRC64;
 Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;
 Oy 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 Db 242 EPERDEVMRYI-LTFLNSVNTMGFIVEDEIVE 274
 RESULT 32
 ID CACM YEAST STANDARD; PRT; 688 AA.
 AC P80235;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 GN Putative mitochondrial carnitine O-acetyltransferase (EC 2.3.1.7).
 DN Name=YAT1; Ordered locus names=VAR035W;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NX NCBI_TaxId=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=DL-1;
 RX MEDLINE=9408564; PubMed=8262985;
 RA Schmalix W., Bandlow W.,
 RT "The ethanol-inducible YAT1 gene from yeast encodes a presumptive
 RT mitochondrial outer carnitine acetyltransferase."
 RL J. Biol. Chem. 268:27428-27439(1993).
 RN (2)
 SQ SEQUENCE FROM N.A.

QY 7 EDNCINFAVAMKFDINTLYFIA--EDDENTLAS 35
 DB 303 EDNCYDIYERKKNNGNINIFCPSDYEDDNNLTLS 333

RESULT 26

ID 0873J5 PRELIMINARY; PRT; 1106 AA.
 AC 0873J5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Probable ATP dependent RNA helicase.
 GN Name=89B11.040;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hehseisel J., Brandt P., Partmann B., Holland R.,
 RA Nykatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL/ BX284747; CAD70310.1; -
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR011545; DEAD/DEAH N.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 KM ATP-binding; Helicase; Hydrolyase.
 SQ SEQUENCE 1106 AA; 124482 MW; B82262FFB78D22A2 CRC64;

Query Match 29.8%; Score 56; DB 2; Length 1106;
 Best Local Similarity 41.4%; Pred. No. 68;
 Matches 12; Conservative 6; Mismatches 7; Indels 4; Gaps 1;
 QY 5 EVEDNCINFAVAMKFDINTLYFIADDDENL 33
 DB 468 PDEBNMWN---KVFNALASISDDKDL 492

RESULT 27

ID 0997A3 PRELIMINARY; PRT; 275 AA.
 AC 0997A3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lysophospholipase homolog.
 GN OrderedLocusNames=SAV1765;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Imai Y., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani U. Y., Takahashi N. K., Sawano T., Inoue K.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogatawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).
 DR EMBL/ AP003363; BAB57927.1; -
 DR PIR/ G89961; G89961.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro: IPR003089; AB hydrolyase.
 DR InterPro: IPR000379; Ser_estrs.
 DR PRINTS: PRO0111; ABHYDROLASE.
 KM Complete proteome.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;

Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;

QY 4 EVEDNCINFAVAMKFDINTLYFIADDDENL 34
 DB 242 EPERDEVMRYI-LTFINNSVNTGFIYEDDEIVE 274

RESULT 28

ID 07A0L7 PRELIMINARY; PRT; 275 AA.
 AC 07A0L7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MM1706 protein.
 GN OrderedLocusNames=MM1706;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL/ AP004828; BAB5571.1; -
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro: IPR003089; AB hydrolyase.
 DR InterPro: IPR000379; Ser_estrs.
 DR PRINTS: PRO0111; ABHYDROLASE.
 KM Complete proteome.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;

Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;

QY 4 EVEDNCINFAVAMKFDINTLYFIADDDENL 34
 DB 242 EPERDEVMRYI-LTFINNSVNTGFIYEDDEIVE 274

RESULT 29

ID 07A5I3 PRELIMINARY; PRT; 275 AA.
 AC 07A5I3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE SA1584 protein.
 GN OrderedLocusNames=SA1584;
 OS Staphylococcus aureus (strain N315).


```

FT NON_TER 1 1
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B89ACB497 CRC64;

Query Match
Best Local Similarity 81.0%; Score 93; DB 2; Length 178;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MKPNDTLYFVAEDDENSED 36
DB 1 MKPNDTLYFVAEDDENSED 21

RESULT 23
ID 096244 PRELIMINARY; PRT; 1643 AA.
AC 096244;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DB Hypothetical protein PF80755W.
GN Name=PF80755W;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
RA Gardner M.J., Tetteh H., Carnucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Ascon C., Lal Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Frazer C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Science 282:1126-1132(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung B., White O., Bertman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Valdiva A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carnucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Frazer C.M., Bartell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL, AE001416; AAC71940.2; -.
DR PIR, H71606; H71606.
KM Hypothetical protein.
SQ SEQUENCE 1643 AA; 19775 MW; DDD2A3B3746B419 CRC64;

Query Match
Best Local Similarity 33.2%; Score 62.5; DB 2; Length 1643;
Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

Qy 4 EPVEDNCINFVAMKFI-----DNTLYFVAEDDENSES 35
DB 1045 EKDLRCISYLSIKNIHIVIKMNMLFYITRDENIS 1085

RESULT 24
ID 07RJW4 PRELIMINARY; PRT; 1153 AA.
AC 07RJW4;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Dentin staphosphoprotein precursor.

```

```

GN Name=PY03111;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kool J.T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush U., Sedegah M., Shoatbi A., Cummings L.M.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdiva A.B.,
RA Van Lin L.H., Jase C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carnucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDA whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, AAE010086; EAA22673.1; -.
SQ SEQUENCE 1153 AA; 135640 MW; ACFCE2E7D3D180E1 CRC64;

Query Match
Best Local Similarity 31.9%; Score 60; DB 2; Length 1153;
Matches 12; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 4 EPVEDNCINFVAMKFI-----DNTLYFVAEDDENSED 36
DB 8 EPKXKNCISNFKXVNMKFEKXNKVLEDD 40

RESULT 25
ID 08IJ91 PRELIMINARY; PRT; 995 AA.
AC 08IJ91;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-UN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF10_0308;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung B., White O., Bertman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Valdiva A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carnucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Frazer C.M., Bartell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL, AE014834; AAN35505.1; -.
DR InterPro, IPR003323; OTU.
DR Pfam, PF02338; OTU.
DR PROSITE, PS50802; OTU.
KM Hypothetical protein.
SQ SEQUENCE 995 AA; 118995 MW; C691E7E47DB52B30 CRC64;

Query Match
Best Local Similarity 30.3%; Score 57; DB 2; Length 995;
Matches 12; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

```

CC Sigmmodon.
 CC NCBI_TaxID=42415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:14980081; DOI=10.1089/107999004772719873;
 RA Bianco J.C., Plecneva L., Boukhalova M., Richardson J.Y.,
 Harris K.A., Prince G.A.;
 RT "The cotton rat: an underutilized animal model for human infectious
 diseases can now be exploited using specific reagents to cytokines,
 chemokines, and interferons."
 RT J. Interferon Cytokine Res. 24:21-28 (2004).
 DR EMBL: AY059406; AAL26703.1;
 DR HSP: Q14116; 1J0S.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005149; P:interleukin-1 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;
 Query Match 58.5%; Score 110; DB 2; Length 196;
 Best Local Similarity 63.9%; Pred. No. 1.6e-07;
 Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 MAAPVEDNCINFAVAMKFIIDNTLYFIAPDDELTESD 36
 Db 2 IAAATPESGSCIFRMTIDNTLYFIPEDNGLSD 37
 RESULT 21
 ID IL18 RAT STANDARD; PRT; 194 AA.
 AC P97636; O88749; P97637;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 25-OCT-2004 (Rel. 45; Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IRN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18; Synonyms=Igf1;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=97152963; PubMed=8999896; DOI=10.1074/jbc.272.4.2035;
 RA Condi B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
 RT "Induction of interferon-gamma inducing factor in the adrenal
 cortex."
 RT J. Biol. Chem. 272:2035-2037 (1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98368130; PubMed=9702748;
 RA Culhane A.C., Hall M.D., Rothwell N.J., Lusheshi G.N.;
 RT "Cloning of rat brain interleukin-18 cDNA."
 RT Mol. Psychiatry 3:362-366 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=New England Deaconess Hospital; TISSUE=Adrenal gland;
 RA Kim S.-J., Kim C.-S., Song K.-Y., Kim U.-S., Jung K.-S.;
 RT "Cloning of the cDNA for interleukin-18 in PC12 and expression in
 Escherichia coli."
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type I
 cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=Beta;
 CC IsoId=P97636-1; Sequence=Displayed;
 CC Name=Alpha;

CC CC IsoId=P97636-2; Sequence=VSP_002659;
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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CC EMBL: U77776; AAC53009.1; -
 CC EMBL: U77777; AAC53010.1; -
 CC EMBL: AJ222813; CAAL1001.1; -
 CC EMBL: AY258448; AAP14669.1; -
 CC DR RGD; 2889; 1118.
 CC DR GO: GO:0005576; C:extracellular; ISS.
 CC DR GO: GO:0005125; P:cytokine activity; ISS.
 CC DR GO: GO:0001525; P:angiogenesis; ISS.
 CC DR GO: GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.
 CC DR GO: GO:0042095; P:interferon-gamma biosynthesis; ISS.
 CC DR GO: GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
 CC DR GO: GO:0030155; P:regulation of cell adhesion; ISS.
 CC DR GO: GO:0045188; P:regulation of circadian sleep/wake cycle, n. .; TBS.
 CC DR GO: GO:0030431; P:sleep; IDA.
 CC DR InterPro; IPR008996; Cytok IL1 like.
 CC DR InterPro; IPR000975; Interleukin_1.
 CC DR Pfam; PF00340; IL1; 1.
 CC DR SMART; SM00125; IL1; 1.
 CC KM Alternative splicing; Cytokine.
 CC FT PROPEP 1 36 By similarity.
 CC FT CHAIN 37 194 Interleukin-18.
 CC FT VARSPLIC 121 139 Missing (in isoform Alpha).
 CC FT FRID 4 5 MS -> IP (in Ref. 2).
 CC FT CONFLICT 48 48 I -> M (in Ref. 2).
 CC FT SEQUENCE 194 AA; 22503 MW; E2089AD5F1798450 CRC64;
 Query Match 58.0%; Score 109; DB 1; Length 194;
 Best Local Similarity 61.1%; Pred. No. 2.2e-07;
 Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 MAAPVEDNCINFAVAMKFIIDNTLYFIAPDDELTESD 36
 Db 1 MAAPVEDNCINFAVAMKFIIDNTLYFIPEDNGLSD 36
 RESULT 22
 ID Q9WZL8 PRELIMINARY; PRT; 178 AA.
 AC Q9WZL8;
 DT 01-OCT-2000 (TrEMBL; Rel. 15; Created)
 DT 01-OCT-2000 (TrEMBL; Rel. 15; Last sequence update)
 DT 01-OCT-2003 (TrEMBL; Rel. 25; Last annotation update)
 DE Interleukin-18 (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC EMBL: AF173175; AAF89833.1; -
 CC DR HSP; Q14116; 1J0S.
 CC DR GO: GO:0005576; C:extracellular; IEA.
 CC DR GO: GO:0005149; P:interleukin-1 receptor binding; IEA.
 CC DR GO: GO:0006955; P:immune response; IEA.
 CC DR InterPro; IPR008996; Cytok IL1 like.
 CC DR InterPro; IPR000975; Interleukin_1.
 CC SMART; SM00125; IL1; 1.

AC P70380, (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DB (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma)
 GN Name=IL18; Synonyms=IGIF;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=96061009; PubMed=7477296; DOI=10.1038/37808a0;
 RA Okamura H., Taniuchi H., Komatsu T., Yutendo M., Hakura A., Tanimoto T.,
 RA Toriige K., Okura T., Nukada Y., Hattori K., Akita K., Namba M.,
 RA Tanabe F., Konishi K., Fukuda S., Kurimoto M.,
 RT Cloning of a new cytokine that induces IFN-gamma production by T
 RT cells.
 RL Nature 378:88-91 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsuki S., Caramori P., Prange C.,
 RA Raba S.S., Loguigno N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Kitzwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schell J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 1-191 FROM N.A.
 RC STRAIN=NOD; TISSUE=Pancreas;
 RX MEDLINE=97174346; PubMed=9022080;
 RA Roche H., Jenkins N.A., Copeland N.G., Kolb H.,
 RT "Active stage of autoimmune diabetes is associated with the expression
 RT of a novel cytokine, IGIF, which is located near Id4."
 RL J. Clin. Invest. 99:469-474 (1997).
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type I
 CC cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 DR EMBL: D49949; BAA08705.1; -
 DR EMBL: BC024384; AA04384.1; -
 DR EMBL: U66344; AB049753.1; -
 DR PIR: S60226; S60226;
 DR MGI: MGI:107936; IL18.
 DR GO: GO:0005576; C:extracellular; ISS.

DR GO: GO:0005125; P:cytokine activity; ISS.
 DR GO: GO:0001525; P:angiogenesis; ISS.
 DR GO: GO:0042033; P:macrophage colony-stimulating f.; ISS.
 DR GO: GO:0042253; P:granulocyte macrophage colony-stimulating f.; ISS.
 DR GO: GO:0008625; P:induction of apoptosis via death domain rec.; TAS.
 DR GO: GO:0042095; P:interferon-gamma biosynthesis; IMP.
 DR GO: GO:0042231; P:interleukin-13 biosynthesis; TAS.
 DR GO: GO:0042094; P:interleukin-2 biosynthesis; ISS.
 DR GO: GO:0003104; P:positive regulation of activated T-cell pro.; ISS.
 DR GO: GO:0030155; P:regulation of cell adhesion; ISS.
 DR GO: GO:0030431; P:sleep; ISS.
 DR InterPro: IPR008996; Cytok IL1 like.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1_1.
 DR SMART: SM00125; IL1_1.
 KM Cytokine; Direct protein sequencing.
 FT PROPER 1 35
 FT CHAIN 36 192 Interleukin-18.
 FT CONFLICT 183 185 MFT -> IS (in Ref. 3).
 SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
 Query Match 58.5%; Score 110; DB 1; Length 192;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINFVAKKFTDNTLYPIAEDDENLESD 36
 DB 6 EDSVNFKEMKFTDNTLYPIEENGDESD 35
 ID 06US06 PRELIMINARY; PRT; 192 AA.
 AC 06US06;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Interleukin 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss; TISSUE=Liver;
 RA Tan Y., Shi Y., Lin L., Pang Y., Xu S., Duan X.,
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY362457; AA063045.1; -
 DR GO: GO:0006955; P:immune response; TAS.
 DR InterPro: IPR008996; Cytok IL1 like.
 SQ SEQUENCE 192 AA; 22075 MW; 8FED9399D0C24491 CRC64;
 Query Match 58.5%; Score 110; DB 2; Length 192;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINFVAKKFTDNTLYPIAEDDENLESD 36
 DB 6 EDSVNFKEMKFTDNTLYPIEENGDESD 35
 ID 091266 PRELIMINARY; PRT; 196 AA.
 AC 091266;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Sigmodon hispidus (Hispid cotton rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

QY 1 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 36
 DB 1 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 36

RESULT 15
 IL18 CANFA STANDARD; PRT; 193 AA.

AC 09XSR01.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DS (Interferon-gamma inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18; Synonyms=IGIF;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=99309818; PubMed=10380699; DOI=10.1007/s002510050532;
 RA Argyile D.J., McGillivray C., Nicolson L., Onions D.E.;
 RT "Cloning, sequencing, and characterization of dog interleukin-18."
 RL Immunogenetics 49:541-543(1999).
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type 1
 CC cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.

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CC EMBL; Y11133; CA72015.1;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0042033; P:chemokine biosynthesis; TAS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec.; IEP.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro.; ISS.
 DR InterPro; IPR008996; Cytok_IL1_1like.
 KM Cytochrome.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22037 MW; 0D97BE586F461F25 CRC64;

Query Match 72.3%; Score 136; DB 1; Length 193;
 Best Local Similarity 72.2%; Pred. No. 2.8e-11;
 Matches 26; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 36
 DB 1 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 36

RESULT 16
 ID 080Y07 PRELIMINARY; PRT; 195 AA.

DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.
 OX NCBI_TaxID=10047;
 RN [1]

SEQUENCE FROM N.A.
 RP TISSUE=Peritoneum;
 RX MEDLINE=22593022; PubMed=12706898; DOI=10.1016/S0378-1119(03)00457-8;
 RA Gaucher D., Chadee K.;
 RT "Gerbil interleukin-18 and caspase-1: cloning, expression and
 RT characterization."
 RL Gene 307:159-166(2003).
 CC -1- SIMILARITY: Belongs to the IL-1 family.

EMBL; AY095932; AA03434.1;
 DR HSSP; Q14116; 100S.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL1_1like.
 DR InterPro; IPR009975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 195 AA; 22172 MW; C6F815317953154D CRC64;

Query Match 64.4%; Score 121; DB 2; Length 195;
 Best Local Similarity 66.7%; Pred. No. 4.1e-09;
 Matches 24; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 36
 DB 2 MAAPVEDNCINFAVAKFIDNTLYFIADDENLSD 37

RESULT 17
 ID 080S88 PRELIMINARY; PRT; 189 AA.

AC 080S88;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=B10.S/DvTe, and SUI/0; TISSUE=Spleen;
 RA Geo J., Teuscher C.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the IL-1 family.

EMBL; AY157834; AA021309.1;
 DR EMBL; AY157835; AA021310.1;
 DR HSSP; Q14115; 100S.
 DR MGD; MGI:107936; IL18.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR008996; Cytok_IL1_1like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 189 AA; 21862 MW; E8F9E5EC0186465 CRC64;

Query Match 58.5%; Score 110; DB 2; Length 189;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFAVAKFIDNTLYFIADDENLSD 36
 DB 3 EDNCINFAVAKFIDNTLYFIADDENLSD 32

RESULT 18
 ID IL18_MOUSE STANDARD; PRT; 192 AA.

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAEPV-DNCISFVEMKFIINTLYFAVENDDELESD 35

RESULT 11
 IL18_BOVIN STANDARD, PRT, 193 AA.

AC 09T073;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN (1)

RP SEQUENCE FROM N.A.
 RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/10799909933118;
 RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
 RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
 18 expression in macrophages and its IFN-gamma-inducing activity."
 RT J. Interferon Cytokine Res. 19:1169-1177(1999).
 RL -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type I
 cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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 or send an email to license@isb-sib.ch).

CC EMBL: AF124789; AAP06686.1; -
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 DR SMART: SM00125; IL1; 1.
 DR CycloKine.
 KW PROPERP
 FT CHAIN 37 193 By similarity.
 FT PROPEP 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 77.7%; Score 146; DB 1; Length 193;
 Best Local Similarity 77.8%; Pred. No. 1e-12;
 Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAEPVEDCISFVEMKFIINTLYFAVENDDELESD 36

RESULT 12
 O6TLW4 PRELIMINARY, PRT, 193 AA.

AC 06TLW4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 NCBI_TaxID=89462;
 RN (1)

RP SEQUENCE FROM N.A.
 RX PubMed=10547157; DOI=10.1089/10799909933118;
 RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
 RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
 18 expression in macrophages and its IFN-gamma-inducing activity."
 RT J. Interferon Cytokine Res. 19:1169-1177(1999).
 RL -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type I
 cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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 or send an email to license@isb-sib.ch).

CC EMBL: AF124789; AAP06686.1; -
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 DR SMART: SM00125; IL1; 1.
 DR CycloKine.
 KW PROPERP
 FT CHAIN 37 193 By similarity.
 FT PROPEP 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 77.7%; Score 146; DB 1; Length 193;
 Best Local Similarity 77.8%; Pred. No. 1e-12;
 Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

RN (1)
 RP SEQUENCE FROM N.A.
 RA Chaudhuri P., Bera B.C.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY394479; AA094552.1; -
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;

Query Match 77.7%; Score 146; DB 2; Length 193;
 Best Local Similarity 77.8%; Pred. No. 1e-12;
 Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAEPVEDCISFVEMKFIINTLYFAVENDDELESD 36

RESULT 13
 O95M33 PRELIMINARY, PRT, 192 AA.

AC 095M33;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Interferon-gamma inducing factor.
 GN Name=IGIF;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN (1)

RP SEQUENCE FROM N.A.
 RA Hanlon L., McGilivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y13923; CAC42918.1; -
 DR HSP: Q4116; 1J08.
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 76.3%; Score 143.5; DB 2; Length 192;
 Best Local Similarity 77.8%; Pred. No. 2.3e-12;
 Matches 28; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAEPVEDCINPVAMKFIIDNTLYFAVENDDELESD 35

RESULT 14
 O6T573 PRELIMINARY, PRT, 193 AA.

AC 06T573;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Interleukin-18.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 NCBI_TaxID=89462;
 RN (1)

RP SEQUENCE FROM N.A.
 RX PubMed=10547157; DOI=10.1089/10799909933118;
 RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
 RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
 18 expression in macrophages and its IFN-gamma-inducing activity."
 RT J. Interferon Cytokine Res. 19:1169-1177(1999).
 RL -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type I
 cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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 or send an email to license@isb-sib.ch).

CC EMBL: AF124789; AAP06686.1; -
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 DR SMART: SM00125; IL1; 1.
 DR CycloKine.
 KW PROPERP
 FT CHAIN 37 193 By similarity.
 FT PROPEP 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22190 MW; 93103B5C62B745DB CRC64;

Query Match 75.5%; Score 142; DB 2; Length 193;
 Best Local Similarity 75.0%; Pred. No. 3.8e-12;
 Matches 27; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 1 MAABVED-CINPVEKFIINTLYFVABNDEDESD 35

RESULT 8
IL18_PIG STANDARD; PRT; 192 AA.

AC 019073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
GN (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
OS Name-IL18; Synonym-IGIF;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Muttanah M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fourtout S., Dozidis C.M., Yerie M., Faltbrother J.M.,
RA Oswald B., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT p15 Interleukin-18";
RL Immunogenetics 51:358-365(2000).
CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
DR EMBL; U68701; AAC18415.1;
DR EMBL; Y11132; CA272014.1;
DR EMBL; AB010003; BAA24135.1;
DR EMBL; AF191088; AAF71200.1;
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec.; IDA.
DR GO; GO:0042035; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro.; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KM Cytokine.
FT PROPEP 1 35 By similarity.
FT CHAIN 36 192 Interleukin-18.
SQ SEQUENCE 192 AA; 22026 MW; 881E654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
Best Local Similarity 80.6%; Pred. No. 6.1e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 MAABVED-CINPVEKFIINTLYFVABNDEDESD 35

RESULT 9
IL18_PIG PRELIMINARY; PRT; 192 AA.

AC 09N1P7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin-18.
GN Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Muttanah M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE=Lung;
RX MEDLINE=20356335; PubMed=10901174;
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
RT "Cloning, sequencing, and expression of porcine interleukin-18 in
RT RT Escherichia coli";
RL Mol. Cells 10:343-347(2000).
DR EMBL; AF176949; AAF35169.1;
DR HSBP; Q14116; I00S.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 78.5%; Score 147.5; DB 2; Length 192;
Best Local Similarity 80.6%; Pred. No. 6.1e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 MAABVED-CINPVEKFIINTLYFVABNDEDESD 35

RESULT 10
IL18_PIG PRELIMINARY; PRT; 177 AA.

AC 06STL7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin 18.
GN Name-IL-18;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu X., Hui L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY50287; AAR27432.1;
DR InterPro; IPR008996; Cytok IL1 like.
SQ SEQUENCE 177 AA; 20300 MW; 426F30330EB1F815 CRC64;

Query Match 77.9%; Score 146.5; DB 2; Length 177;
Best Local Similarity 80.6%; Pred. No. 7.8e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

AC 09X807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DB (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18; Synonyms=IGIF;
 OS Equus caballus (Horse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nicolson L., Peña-Gonzales M.N., Keanie J.L., Logan N.A.,
 RA Artye D.J., Orlons D.E.;
 RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs."
 RL Submitted (FE8-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type 1
 cells (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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 CC
 CC EMBL; Y1131; CAA72013.1;
 DR InterPro; IPR008996; Cyclo_IL1_1like.
 KW CycloIL1.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22058 MW; 4D8153559004BECF CRC64;
 QY
 Query Match 84.6%; Score 159; DB 1; Length 193;
 Best Local Similarity 83.3%; Pred. No. 1,4e-14;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCISFVEMKFIIDNTLYFAEDDENLESD 36
 RESULT 5
 ID 06WUJ7 PRELIMINARY; PRT; 189 AA.
 AC 06WUJ7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE DELTA3PRO-IL-18.
 GN Name=IL18;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gaggero A., De Ambrosio A., Mezzananza D., Piazza T., Rubartelli A.,
 RA Fagiani M., Canevari S., Parrini S.;
 RT "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
 resistant to caspase-1 and -4 processing."
 RL Oncogene 0:0-0(2004).
 DR EMBL; AY266351; AAP92112.1;
 DR InterPro; IPR008996; Cyclo_IL1_1like.
 SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF73JA4B6 CRC64;
 QY
 Query Match 82.4%; Score 155; DB 2; Length 189;
 Best Local Similarity 88.9%; Pred. No. 5e-14;

Matches 32; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 OY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCISFVEMKFIIDNTLYFAEDDENLESD 32
 RESULT 6
 ID 09GL09 PRELIMINARY; PRT; 193 AA.
 AC 09GL09;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Interleukin-18 (IGIF).
 GN Name=IL-18;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bailey S.L., Gosner A., Dalziel R., Hopkins J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401033; CAC09326.2; -.
 DR HSP; Q1416; 1J08.
 DR GO; GO:0005576; Cextracellular; IEA.
 DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cyclo_IL1_1like.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1_1.
 SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EP18C CRC64;
 QY
 Query Match 82.4%; Score 155; DB 2; Length 193;
 Best Local Similarity 80.6%; Pred. No. 5.1e-14;
 Matches 29; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCISFVEMKFIIDNTLYFAEDDENLESD 36
 RESULT 7
 ID 0865B8 PRELIMINARY; PRT; 192 AA.
 AC 0865B8;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE Interferon gamma inducing factor precursor.
 GN Name=fil-18;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawanara C., Kawakami K., Kishi M., Mochizuki M.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056857; BAC65243.1; -.
 DR HSP; Q1416; 1J08.
 DR InterPro; IPR008996; Cyclo_IL1_1like.
 KW Signal.
 FT SIGNAL 1 35 Potential.
 SQ SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;
 QY
 Query Match 82.2%; Score 154.5; DB 2; Length 192;
 Best Local Similarity 83.3%; Pred. No. 6e-14;
 Matches 30; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
 OY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36

RA Butterfield V.S.N., Krzywnski M.I., Skalska U., Smalins D.E.,
 RA Scherich A., Schein J.E., Jones S.J.M., Marra N.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." *Nat. Acad. Sci. U.S.A.* 99:16899-16903 (2002).
 RN (5)
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-Peripheral blood.
 RA Contt B., Kim S.J., Tint C., Chun H.S., Joh T.H.,
 RA Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type 1
 CC cells.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 SIMILARITY: Belongs to the IL-1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).

DR EMBL; D49950; BAA08706.1; -
 DR EMBL; AF077611; AAC37287.1; -
 DR EMBL; AY044641; AAK5950.1; -
 DR EMBL; BC007007; AAH07007.1; -
 DR EMBL; BC007461; AAH07461.1; -
 DR EMBL; U90434; AAB50010.1; -
 DR PDB; 1J0S; NMR; A=37-193.
 DR OGP; Q14116; -
 DR Genev; HGNC:5986; IL18.
 DR H-InvDB; HIK0010123; -
 DR MIM; 600953; -
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0001525; P:angiogenesis; IDA.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0042033; P:chemokine biosynthesis; TAS.
 DR GO; GO:0006955; P:granulocyte macrophage colony-stimulating f.; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:0008635; P:induction of apoptosis via death domain rec.; ISS.
 DR GO; GO:0042035; P:interferon-gamma biosynthesis; TAS.
 DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
 DR GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.
 DR GO; GO:0030155; P:positive regulation of activated T-cell pro.; IDA.
 DR GO; GO:0030431; P:sleep; ISS.
 DR GO; GO:0042092; P:T-helper 2 type immune response; TAS.
 DR InterPro; IPR008996; Cytok_IL11ike.
 DR SMART; SM00125; IL1; 1.
 DR 3D-structure; Cytokine.
 FT PROPEP 1 36
 FT CHAIN 37 193 By similarity.
 FT CONFLICT 66 66 Interleukin-18.
 FT CONFLICT 86 86 F -> L (in Ref. 2).
 FT CONFLICT 191 191 S -> R (in Ref. 2).
 FT CONFLICT 191 191 N -> S (in Ref. 2).
 SQ SEQUENCE 193 AA; 22326 MW; 323C62C20378BD55 CRC64;

Query Match 100.0%; Score 188; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.2e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 Db 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 2
 096KJ8

ID 096KJ8 PRELIMINARY; PRT; 193 AA.
 AC 096KJ8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin 18.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ying P., Jianxin L.;
 RA Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF380360; AAK57024.1; -
 DR HSSP; Q14116; 1J0S.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL11ike.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 100.0%; Score 188; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.2e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 Db 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 3
 ID 09BG15 PRELIMINARY; PRT; 193 AA.
 AC 09BG15;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin-18.
 GN Name=IL18;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_Taxid=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2129850; PubMed=11331040; DOI=10.1089/107999001750133212;
 RA Glavetoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
 RA Hodara V.L.;
 RT "Expression of the interleukin-18 gene from rhesus macaque by the
 RT simian immunodeficiency virus does not result in increased viral
 RT replication.";
 RL J. Interferon Cytokine Res. 21:173-180(2001).
 DR EMBL; AF303732; AAK13416.1; -
 DR HSSP; Q14116; 1J0S.
 DR InterPro; IPR008996; Cytok_IL11ike.
 SQ SEQUENCE 193 AA; 22325 MW; B2BD29C03BB05E CRC64;

Query Match 95.2%; Score 179; DB 2; Length 193;
 Best Local Similarity 94.4%; Pred. No. 1.8e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 Db 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 4
 IL18_HORSE STANDARD; PRT; 193 AA.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 12:15:40 / Search time 175 Seconds
(without alignments)
105.342 Million cell updates/sec

Title: US-09-711-896a-1
Perfect score: 188
Sequence: 1 MAAPVEDNCINPVAKPFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot; 2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	188	100.0	193 1 IL18 HUMAN	Q14116 homo sapien
2	188	100.0	193 2 O96KJ8	O96KJ8 homo sapien
3	179	95.2	193 2 O9BG15	O9BG15 macaca mula
4	159	84.6	193 1 IL18 HORSE	O9X877 equus cabal
5	155	82.4	189 2 O6WJ07	O6WJ07 homo sapien
6	155	82.4	193 2 O9GL09	O9GL09 ovine aries
7	154.5	82.2	192 2 O865B8	O865B8 felis silve
8	147.5	78.5	192 1 IL18 PIG	O19073 sus scrofa
9	147.5	78.5	192 2 O9N1P7	O9N1P7 sus scrofa
10	146.5	77.5	193 2 O6STL7	O6STL7 sus scrofa
11	146	77.7	193 1 IL18 BOVIN	O9TUV3 bos taurus
12	146	77.7	193 2 O6TLW4	O6TLW4 bubalus bub
13	143.5	76.3	192 2 O9SM33	O9SM33 felis silve
14	142	75.5	193 2 O6T573	O6T573 bubalus bub
15	136	72.3	193 1 IL18 CANFA	O9X870 canis fami
16	121	64.4	195 2 O80707	O80707 meriones un
17	110	58.5	189 2 O80S88	O80S88 mus musculu
18	110	58.5	192 1 IL18 MOUSE	P70303 mus musculu
19	110	58.5	192 2 O6USQ6	O6USQ6 mus musculu
20	110	58.5	196 2 O91Z66	O91Z66 sigmodon hi
21	109	58.0	194 1 IL18 RAT	P97636 rattus norv
22	93	49.5	178 2 O9WZL8	O9WZL8 bos taurus
23	62.5	33.2	1643 2 O96Z44	O96Z44 plasmodium
24	60	31.9	1163 2 O7RWJ4	O7RWJ4 plasmodium
25	57	30.3	1955 2 O81R71	O81R71 plasmodium
26	56	29.8	1106 2 O873J5	O873J5 neurospora
27	55	29.3	275 2 O997N3	O997N3 staphylococ
28	55	29.3	275 2 O7A017	O7A017 staphylococ
29	55	29.3	275 2 O7A513	O7A513 staphylococ
30	55	29.3	275 2 O6G843	O6G843 staphylococ
31	55	29.3	275 2 O6GFT8	O6GFT8 staphylococ

32	55	29.3	688 1 CACM YEAST	P80235 saccharomyc
33	55	29.3	862 2 O6CUT7	O6CUT7 kluyveromyc
34	54.5	29.0	439 2 O7Q5F7	O7Q5F7 anopheles g
35	54	28.7	417 2 O96410	O96410 hydra atten
36	54	28.7	921 2 O7YZ56	O7YZ56 cryptospori
37	53.5	28.5	494 2 O86A22	O86A22 dictyostell
38	53.5	28.5	1055 2 O6S146	O6S146 african swi
39	53	28.2	70 2 O9JN03	O9JN03 campylobact
40	53	28.2	99 2 O776W7	O776W7 bacterioph
41	53	28.2	298 2 O858S2	O858S2 bacterioph
42	53	28.2	365 2 O9PNP3	O9PNP3 campylobact
43	53	28.2	956 2 O7RG03	O7RG03 plasmodium
44	53	28.2	1039 2 O9CV97	O9CV97 toxoplasma
45	52.5	27.9	130 2 O6MKQ3	O6MKQ3 bdellovibri

ALIGNMENTS

RESULT 1	IL18 HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116, 075599,			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)			
DE	(IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).			
GN	Name=IL18; Synonyms=IGIF			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96247646; PubMed=8666798;			
RA	Ushio S., Namba M., Okura T., Hattori K., Mukada Y., Akita K.,			
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,			
RA	Pukuda S., Ikeda M., Okamura H., Kurimoto M.;			
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression			
RT	in Escherichia coli, and studies on the biologic activities of the			
RT	protein.";			
RL	J. Immunol. 156:4274-4279 (1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Tong D., Guixin D., Lihua H., Haitao W.;			
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";			
RT	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RT	"Cloning of human interleukin 18 cDNA.";			
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Urinary bladder;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899.			
RA	Krausberger R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA	Stausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.B., Casavant J.L., Scheetz T.E.,			
RA	Browstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abaxsson R.D., Mullaly S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallien D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley M., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,610
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR FILING DATE: 2000-09-06
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PERL Program
SEQ ID NO 363
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incyle ID No: LG:1015157.1.orfl:2000SEP08
US-10-363-829-363

Query Match
Best Local Similarity 45.5%; Score 49.5; DB 16; Length 185;
Matches 10; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKFIIDNTLYFIADDDEN 32
DB 62 LDFPSMKF---SLYFLAYEDKN 80

RESULT 39
US-10-369-493-13822
Sequence 13822, Application US/10369493
Publication No: US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfang
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13822
LENGTH: 380
TYPE: PRT
ORGANISM: Pseudomonas fluorescens
US-10-369-493-13822

Query Match
Best Local Similarity 37.5%; Score 49.5; DB 15; Length 380;
Matches 12; Conservative 3; Mismatches 16; Indels 1; Gaps 1;

QY 2 AAEFVEDNCINFVAMKFIIDNTLYFIADDDEN 33
DB 205 AANPITDACA-LKAMTLISNNLRLLVVRDGSGL 235

RESULT 40
US-10-363-616-488
Sequence 488, Application US/10363616
Publication No: US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hvaeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 488

LENGTH: 547
TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-616-488

Query Match
Best Local Similarity 39.4%; Score 49.5; DB 15; Length 547;
Matches 13; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 7 EDNCINFVAMKFIIDNTLY---FIADDDENLESD 36
DB 315 EDGCIIVFDVIAVEDNSLYQLFYLA---NLNOD 343

Search completed: May 13, 2005, 12:38:10
Job time : 135 secs

Db 308 ISSDPMEDVCCQLYTRFISNTI 330

RESULT 35
US-10-087-167-14

/ Sequence 14, Application US/10087167
/ Publication No. US20030154509A1
/ GENERAL INFORMATION:
/ APPLICANT: Pascal, Erica
/ APPLICANT: Valentine, Scott
/ APPLICANT: Brown, Jeffrey
/ APPLICANT: Cockrell, Adam
/ APPLICANT: Johnson, Brian
/ TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
/ FILE REFERENCE: 50018A
/ CURRENT APPLICATION NUMBER: US/10/087,167
/ PRIOR FILING DATE: 2002-03-01
/ PRIOR APPLICATION NUMBER: US 60/242,969
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 14
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: Chironomus tentans
US-10-087-167-14

Query Match 26.6%; Score 50; DB 14; Length 536;
Best Local Similarity 38.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 11 INFVANKPFDNTLYFAEDDENLESD 36
Db 16 LNVASQSPGDNNITYGATKKQRLSESD 41

RESULT 36
US-10-606-060A-9

/ Sequence 9, Application US/10606060A
/ Publication No. US20040058369A1
/ GENERAL INFORMATION:
/ APPLICANT: Syngenta
/ APPLICANT: Jepsen, Ian
/ APPLICANT: Martinez, Alberto
/ APPLICANT: Greenland, Andrew James
/ TITLE OF INVENTION: A GENE SWITCH
/ FILE REFERENCE: 1392/4/3/2
/ CURRENT APPLICATION NUMBER: US/10/606,060A
/ PRIOR FILING DATE: 2003-06-25
/ PRIOR APPLICATION NUMBER: US 08/553,648
/ PRIOR FILING DATE: 1996-05-24
/ PRIOR APPLICATION NUMBER: US 09/564,418
/ PRIOR FILING DATE: 2000-05-03
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: Chironomus tentans
US-10-606-060A-9

Query Match 26.6%; Score 50; DB 15; Length 536;
Best Local Similarity 38.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 11 INFVANKPFDNTLYFAEDDENLESD 36
Db 16 LNVASQSPGDNNITYGATKKQRLSESD 41

RESULT 37
US-10-437-963-141822

/ Sequence 141822, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yinhua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boulharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 141822
/ LENGTH: 663
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURES:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_4288C.1.pap
US-10-437-963-141822

Query Match 26.6%; Score 50; DB 16; Length 663;
Best Local Similarity 32.1%; Pred. No. 2.4e+02;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AAEPVEDNCINFVANKPFDNTLYFAED 29
Db 206 APEALSLNCVNSGVNVDTGTYWLTED 233

RESULT 38
US-10-363-829-363

/ Sequence 363, Application US/10363829
/ Publication No. US20040142331A1
/ GENERAL INFORMATION:
/ APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
/ APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
/ APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
/ APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
/ APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
/ APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
/ APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
/ APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
/ APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
/ APPLICANT: Gerstl, Jr., Edward H.; Peralta, Careyna H.;
/ APPLICANT: David, Marie H.; Panzer, Scott R.;
/ APPLICANT: Flores, Vincent Z.; Daffo, Abel;
/ APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
/ APPLICANT: Chang, Simon C.; Au, Alan P.;
/ APPLICANT: Inman, Redekah R.
/ TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
/ FILE REFERENCE: PT-1183 USN
/ CURRENT APPLICATION NUMBER: US/10/363,829
/ CURRENT FILING DATE: 2003-03-05
/ PRIOR APPLICATION NUMBER: PCT/US01/27628
/ PRIOR FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: US 60/229,751
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/229,749
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/229,750
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/229,747
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/229,748
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/230,583
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: US 60/230,517

US-10-437-963-150952
Sequence 150952, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 150952
LENGTH: 224
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(224)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_51140C.1.pap
US-10-437-963-150952

Query Match 26.9%; Score 50.5; DB 16; Length 224;
Best Local Similarity 35.7%; Pred. No. 59;
Matches 10; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 5 PVEDNCINFVAMKFIIDNTLYFAEDDEN 32
DB 135 PIEDLCIDPTLPGYPD---YIIEGSEEN 159

RESULT 32
US-10-437-963-150950
Sequence 150950, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 150950
LENGTH: 1083
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_51139C.1.pap
US-10-437-963-150950

Query Match 26.9%; Score 50.5; DB 16; Length 1083;
Best Local Similarity 35.7%; Pred. No. 3.7e+02;
Matches 10; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 5 PVEDNCINFVAMKFIIDNTLYFAEDDEN 32
DB 868 PIEDLCIDPTLPGYPD---YIIEGSEEN 892

RESULT 33
US-09-748-637A-318
Sequence 318, Application US/09749637A
Patent No. US20020173449A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olyvera, Baldomero M.
APPLICANT: Carter, G. Edward
APPLICANT: Watkins, Warren
APPLICANT: Hilliard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Laver, Richard T.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US60/219,440
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/173,754
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PatentIn version 3.0
SEQ ID NO 318
LENGTH: 78
TYPE: PRT
ORGANISM: Conus imperialis
US-09-749-637A-318

Query Match 26.6%; Score 50; DB 9; Length 78;
Best Local Similarity 34.8%; Pred. No. 20;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 10 CINFVAMKFIIDNTLYFAEDDEN 32
DB 5 CVFPAVAFELTASVFTADDSRN 27

RESULT 34
US-10-424-599-174564
Sequence 174564, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174564
LENGTH: 438
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_12864C.1.pap
US-10-424-599-174564

Query Match 26.6%; Score 50; DB 15; Length 438;
Best Local Similarity 34.8%; Pred. No. 1.5e+02;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTL 23

```

US-10-170-385-285
;
; Sequence 285, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: Fastseq for Windows Version 4.0.
; SEQ ID NO 285
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-285

```

RESULT 30.
 US-10-369-493-20614
 Sequence 20614, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ. ID NOS: 47374
 SEQ. ID NO 20614
 LENGTH: 383
 TYPE: PRT
 ORGANISM: Rhodospseudomonas palustris
 US-10-369-493-20614

	Query Match	Similarity	27.4%	Score 51.5	DB 15	Length 389
Dc	Best Local	Similarity	36.4% <td>Pred No. 79</td> <td></td> <td></td>	Pred No. 79		
	Matches	12	Conservative	6	Mismatches	14
					Indels	1
					Gaps	1
Cy	1	MAAEPEEDNCINFVAMKFIIDNTLYFIADDDENTL	33			
	:	: : :	:	:	:	:
Dc	206	IATPITDACA-LKAMGIISLSLTVAACQNL	237			

RESULT 31

```

PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33630
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000241.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.9
OTHER INFORMATION: EST HUMAN HIT: A1652927.1, EVALU8 9.00e-25
OTHER INFORMATION: SWISSPROT HIT: O14867, EVALU8 2.00e-89
OTHER INFORMATION: EST_HUMAN HIT: A0134963.1, EVALU8 1.00e-69
US-09-864-761-33630.

Query Match 27.7% Score 52; DB 9; Length 156;
Best Local Similarity 31.8%; Pred. No. 24;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 MAAPVEDNCINPAMKFIINT 22
Db 12 LSVNHIESCFQFLKFKFLDST 33

RESULT 27
US-09-864-761-46601
Sequence 46601, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheing
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Acomica-X-1
```

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46601
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000201.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EST HUMAN HIT: A0134963.1, EVALU8 1.00e-130
OTHER INFORMATION: SWISSPROT HIT: O14867, EVALU8 0.00e+00
US-09-864-761-46601

Query Match 27.7% Score 52; DB 9; Length 445;
Best Local Similarity 31.8%; Pred. No. 80;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 MAAPVEDNCINPAMKFIINT 22
Db 35 LSVNHIESCFQFLKFKFLDST 56

RESULT 28
US-09-864-761-47605
Sequence 47605, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
```

APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 1397
 LENGTH: 687
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-1397

Query Match 29.3%; Score 55; DB 15; Length 687;
 Best Local Similarity 34.5%; Pred. No. 50;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 8 DNCINFVAMKPIDNTLYFIADDENLSD 36
 DB 260 DDCMKNKLDLSALFVCLDVAAPAD 288

RESULT 23
 US-10-872-874-158
 Sequence 158, Application US/10872874
 Publication No. US20050003419A1
 GENERAL INFORMATION:
 APPLICANT: Breves, Roland
 APPLICANT: Maurel, Karl-Heinz
 APPLICANT: Eck, Jurgen
 APPLICANT: Lorenz, Patrick
 APPLICANT: Zinke, Holger
 TITLE OF INVENTION: GLYCOSYL HYDROLASES
 FILE REFERENCE: HENK-0088 / H 5206
 CURRENT APPLICATION NUMBER: US/10/872,874
 CURRENT FILING DATE: 2004-06-21
 PRIOR APPLICATION NUMBER: PCT/EP02/14210
 PRIOR FILING DATE: 2002-12-13
 PRIOR APPLICATION NUMBER: DE 101 63 748.9
 PRIOR FILING DATE: 2001-12-21
 NUMBER OF SEQ ID NOS: 320
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 158
 LENGTH: 81
 TYPE: PRT
 ORGANISM: Streptomyces coelicolor
 US-10-872-874-158

Query Match 28.7%; Score 54; DB 16; Length 81;
 Best Local Similarity 43.5%; Pred. No. 5.8;
 Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 14 VAMKPIDNTLYFIADDENLSD 36
 DB 20 VSLKIDNTLYFIADDENLSD 42

RESULT 24
 US-10-369-493-11186
 Sequence 1186, Application US/10369493
 Publication No. US2003023675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 11186
 LENGTH: 679
 TYPE: PRT
 ORGANISM: Methanococcus marisnigri
 US-10-369-493-11186

FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 11186
 LENGTH: 679
 TYPE: PRT
 ORGANISM: Methanococcus marisnigri
 US-10-369-493-11186

Query Match 28.2%; Score 53; DB 15; Length 679;
 Best Local Similarity 37.9%; Pred. No. 94;
 Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

OY 8 DNCINFVAMKPIDNTLYFIADDENLSD 36
 DB 272 DNLGVPFSPKIDNTLYFIADDENLSD 300

RESULT 25
 US-09-764-864-1231
 Sequence 1231, Application US/09764864
 Patent No. US20020132753A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT23
 CURRENT APPLICATION NUMBER: US/09/764,864
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 1792
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1231
 LENGTH: 151
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (148)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-864-1231

Query Match 27.7%; Score 52; DB 9; Length 151;
 Best Local Similarity 31.8%; Pred. No. 23;
 Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 MAEPVEDNCINFVAMKPIDNT 22
 DB 122 LSVNIBSCFOFLKPKFLDST 143

RESULT 26
 US-09-864-761-33630
 Sequence 33630, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aecmics-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03

DB 6 EDCSCNFKEMFIDNTLYFIPEBNGDLESD 35

RESULT 18
US-10-895-396-12
Sequence 12, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephane
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 033751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: fusion murine IL-2/linker/murine pro IL-18
US-10-895-396-12

Query Match 58.5%; Score 110; DB 17; Length 371;
Best Local Similarity 66.7%; Pred. No. 4,4e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFVAMKFIDNTLYFIADDDNLESD 36
DB 185 EDCSCNFKEMFIDNTLYFIPEBNGDLESD 214

RESULT 19
US-10-895-396-13
Sequence 13, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephane
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: fusion murine IL-2/linker/murine pro IL-18 K69A
US-10-895-396-13

Query Match 58.5%; Score 110; DB 17; Length 371;
Best Local Similarity 66.7%; Pred. No. 4,4e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFVAMKFIDNTLYFIADDDNLESD 36
DB 185 EDCSCNFKEMFIDNTLYFIPEBNGDLESD 214

RESULT 20
US-10-369-493-3839
Sequence 3839, Application US/10369493

Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3839
LENGTH: 1116
TYPE: PRT
ORGANISM: Neurospora crassa
FEATURES:
NAME/KEY: unsure
LOCATION: (1) (1116)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3839

Query Match 29.8%; Score 56; DB 15; Length 1116;
Best Local Similarity 41.4%; Pred. No. 64;
Matches 12; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 5 PVEDNCINFVAMKFIDNTLYFIADDDNLESD 33
DB 455 PDEENMVN---KVFENALASLEDDKNTL 479

RESULT 21
US-10-424-599-240517
Sequence 240517, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 240517
LENGTH: 108
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT3847_59214C.1.pcp
US-10-424-599-240517

Query Match 29.5%; Score 55.5; DB 15; Length 108;
Best Local Similarity 32.6%; Pred. No. 5;
Matches 14; Conservative 6; Mismatches 4; Indels 19; Gaps 2;

QY 6 VEDNCINFVAMK---FID-----NTLYFIAD 29
DB 52 VDNDCINFVAMKFWYINRYPTLLCSAKGKTLAVYVED 94

RESULT 22
US-10-369-493-1397
Sequence 1397, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.

PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 133
TYPE: PRT
ORGANISM: Felis catus
FEATURE:
NAME/KEY: misc feature
LOCATION: (119)..(119)
OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
NAME/KEY: misc feature
LOCATION: (470)..(470)
OTHER INFORMATION: n = unknown at position 470
OTHER INFORMATION: Xaa = unknown at position 119
US-09-917-265-2

Query Match 74.2%; Score 139.5; DB 9; Length 133;
Best Local Similarity 75.0%; Pred. No. 9.2e-12;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAPVEDNCINIVAMKFIINTLYPIAEDDENTLSD 36
DB 1 MTAIPVDD-CINIVGKMFIDNTLYPIVADSDENLETD 35

RESULT 15
US-09-917-265-8
Sequence 8, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borowski, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 192
TYPE: PRT
ORGANISM: Felis catus
US-09-917-265-8

Query Match 74.2%; Score 139.5; DB 9; Length 192;
Best Local Similarity 75.0%; Pred. No. 1.4e-11;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAPVEDNCINIVAMKFIINTLYPIAEDDENTLSD 36
DB 1 MTAIPVDD-CINIVGKMFIDNTLYPIVADSDENLETD 35

RESULT 16
US-09-770-528-9
Sequence 9, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kaschelen, Robert A.
TITLE OF INVENTION: Mammalian Cytokines, Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-770-528-9

Query Match 58.5%; Score 110; DB 9; Length 192;
Best Local Similarity 66.7%; Pred. No. 2e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINIVAMKFIINTLYPIAEDDENTLSD 36
DB 6 EDCVNFVKKMFIDNTLYPIFPEENGDLSD 35

RESULT 17
US-10-105-080-5
Sequence 5, Application US/10105080
Publication No. US20030143203A1
GENERAL INFORMATION:
APPLICANT: SANTIANG GENEX CORPORATION
TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Koparentin 1.71
SEQ ID NO 5
LENGTH: 192
TYPE: PRT
ORGANISM: mouse interleukin-18 precursor mutant
US-10-105-080-5

Query Match 58.5%; Score 110; DB 14; Length 192;
Best Local Similarity 66.7%; Pred. No. 2e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINIVAMKFIINTLYPIAEDDENTLSD 36

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 36
 DB 169 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 204

RESULT 10
 US-10-094-153-3
 ; Sequence 3, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-3

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 11
 US-10-094-153-4
 ; Sequence 4, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-4

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 12
 US-10-094-153-5

; Sequence 5, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-5

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 13
 US-10-094-153-9
 ; Sequence 9, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-9

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 14
 US-09-917-265-2
 ; Sequence 2, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Borosha, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 ; FILE REFERENCE: 1W-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27

SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-10-679-201-5

Query Match 100.0%; Score 188; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36

RESULT 6
US-10-646-308-13
Sequence 13, Application US/10646308
Publication No. US20040136992A1
GENERAL INFORMATION:
APPLICANT: BURTON, Paul B. J.
APPLICANT: DEISHER, Theresa A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
FILE REFERENCE: 3432-B
CURRENT APPLICATION NUMBER: US/10/646,308
PRIOR FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: --to be assigned--
PRIOR FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/406,418
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.2
SEQ ID NO 13
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (73)..(73)
OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.
US-10-646-308-13

Query Match 100.0%; Score 188; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36

RESULT 7
US-10-823-964A-3
Sequence 3, Application US/10823964A
Publication No. US2005008615A1
GENERAL INFORMATION:
APPLICANT: BAM, NARENDRA
APPLICANT: BONGERS, JACOB
APPLICANT: KIRKPATRICK, ROBERT B.
APPLICANT: JANSON, CHERYL A.
APPLICANT: JOHANSON, KTRUNG
APPLICANT: QIU, XIANYANG
TITLE OF INVENTION: CONJUGATES COMPRISING HUMAN IL-18 AND
FILE REFERENCE: PUG0053
CURRENT APPLICATION NUMBER: US/10/823,964A
PRIOR FILING DATE: 2004-04-14
PRIOR APPLICATION NUMBER: 60/462,947
PRIOR FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 203
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-964A-3

Query Match 100.0%; Score 188; DB 17; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 46

RESULT 8
US-10-895-396-8
Sequence 8, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephanie
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 361
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion human IL-2/linker/human pro IL-18
US-10-895-396-8

Query Match 100.0%; Score 188; DB 17; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
DB 169 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 204

RESULT 9
US-10-895-396-9
Sequence 9, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephanie
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 361
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion human IL-2/linker/human pro IL-18 K89A
US-10-895-396-9

Query Match 100.0%; Score 188; DB 17; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;

GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Kasteln, Fernando J.
Kasteln, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match 100.0%; Score 188; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36

RESULT 3
US-10-311-491-1
Sequence 1, Application US/10311491
Publication No. US20030143198A1
GENERAL INFORMATION:
APPLICANT: Johnson, Kyung O.
APPLICANT: Kirkpatrick, Robert B.
APPLICANT: Shatzman, Allan R.
APPLICANT: Ho, Yen Sen
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Method for Preparing a Physiologically
Active IL-18 Polypeptide
FILE REFERENCE: P51137
CURRENT APPLICATION NUMBER: US/10/311,491

CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/US01/18804
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/211,832
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/224,128
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/264,923
PRIOR FILING DATE: 2001-01-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapien
US-10-311-491-1

Query Match 100.0%; Score 188; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36

RESULT 4
US-10-105-080-4
Sequence 4, Application US/10105080
Publication No. US20030143203A1
GENERAL INFORMATION:
APPLICANT: SAMYANG GENEX CORPORATION
TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopacentin 1.71
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Human Interleukin-18 precursor mutant
US-10-105-080-4

Query Match 100.0%; Score 188; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36

RESULT 5
US-10-679-201-5
Sequence 5, Application US/10679201
Publication No. US20040120923A1
GENERAL INFORMATION:
APPLICANT: DINARELLO, CHARLES A.
APPLICANT: KIM, SOO-HYUN
APPLICANT: BUFLER, PHILIP
TITLE OF INVENTION: METHOD OF TREATMENT USING A CYTOKINE ABLE TO BIND
TO IL-18BP TO INHIBIT THE ACTIVITY OF A SECOND CYTOKINE
FILE REFERENCE: 057878-000011
CURRENT APPLICATION NUMBER: US/10/679,201
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/416,827
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 3.2

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
89.745 Million cell updates/sec.

Title: US-09-711-896a-1

Perfect score: 1 MAABPVEDNCINFVANKFIDNTLYFAEDDENLESD 36

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Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:
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2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	193	9	US-09-798-075-1
2	188	100.0	193	9	US-09-770-528-8
3	188	100.0	193	14	US-10-311-491-1
4	188	100.0	193	14	US-10-105-080-4
5	188	100.0	193	16	US-10-679-201-5
6	188	100.0	193	16	US-10-646-308-13
7	188	100.0	203	17	US-10-823-964A-3
8	188	100.0	361	17	US-10-895-396-9
9	188	100.0	361	17	US-10-895-396-9
10	176	93.6	193	13	US-10-094-153-3
11	176	93.6	193	13	US-10-094-153-4
12	176	93.6	193	13	US-10-094-153-5
13	176	93.6	193	13	US-10-094-153-9

14	139.5	74.2	133	9	US-09-917-265-2	Sequence 2, Appl1
15	139.5	74.2	132	9	US-09-917-265-8	Sequence 8, Appl1
16	110	58.5	192	9	US-09-770-528-9	Sequence 9, Appl1
17	110	58.5	192	14	US-10-105-080-5	Sequence 5, Appl1
18	110	58.5	371	17	US-10-895-396-12	Sequence 12, Appl1
19	110	58.5	371	17	US-10-895-396-11	Sequence 13, Appl1
20	56	29.8	1116	15	US-10-369-493-3839	Sequence 3839, Ap
21	55.5	29.3	108	15	US-10-424-599-240517	Sequence 240517,
22	55	29.3	687	15	US-10-369-493-1597	Sequence 1597, Ap
23	54	28.7	81	16	US-10-872-874-158	Sequence 158, App
24	53	28.2	679	15	US-10-369-493-11186	Sequence 11186, A
25	52	27.7	151	9	US-09-764-864-1231	Sequence 1231, Ap
26	52	27.7	156	9	US-09-864-761-33630	Sequence 33630, A
27	52	27.7	445	9	US-09-864-761-46601	Sequence 46601, A
28	52	27.7	746	9	US-09-864-761-47605	Sequence 47605, A
29	52	27.7	736	15	US-10-170-385-285	Sequence 285, App
30	51.5	27.4	183	15	US-10-369-493-20614	Sequence 20614, A
31	50.5	26.9	224	16	US-10-437-963-150952	Sequence 150952,
32	50.5	26.9	1083	16	US-10-437-963-150950	Sequence 150950,
33	50	26.6	78	9	US-09-749-637A-318	Sequence 318, App
34	50	26.6	438	15	US-10-424-599-174564	Sequence 174564,
35	50	26.6	536	14	US-10-087-167-14	Sequence 14, Appl1
36	50	26.6	536	15	US-10-606-060A-9	Sequence 9, Appl1
37	50	26.6	663	16	US-10-437-963-111822	Sequence 111822,
38	49.5	26.3	185	16	US-10-363-823-363	Sequence 363, App
39	49.5	26.3	380	15	US-10-369-493-13822	Sequence 13822, A
40	49.5	26.3	547	15	US-10-363-616-488	Sequence 488, App
41	49.5	26.3	568	15	US-10-282-122A-57666	Sequence 57666, A
42	49.5	26.3	285	16	US-10-437-963-134407	Sequence 134407,
43	49	26.1	285	9	US-09-815-242-4869	Sequence 4869, Ap
44	49	26.1	295	15	US-10-282-122A-42529	Sequence 42529, A
45	49	26.1	334	9	US-09-815-242-10798	Sequence 10798, A

ALIGNMENTS

RESULT 1
US-09-798-075-1
Sequence 1, Application US/09798075
Patent No. US2001004418A1
GENERAL INFORMATION:
APPLICANT: Levy, Shoshana
APPLICANT: Dekruiff, Rosemarie
APPLICANT: Umetzu, Dale
APPLICANT: Maecker, Holden
TITLE OF INVENTION: Treatment of Allergies
FILE REFERENCE: STAN-179
CURRENT APPLICATION NUMBER: US/09/798, 075
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/188, 311
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-075-1

Query Match 100.0%, Score 188, DB 9, Length 193,
Best Local Similarity 100.0%, Pred. No. 2, 1e-18,
Matches 36, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
OY 1 MAABPVEDNCINFVANKFIDNTLYFAEDDENLESD 36
DB 1 MAABPVEDNCINFVANKFIDNTLYFAEDDENLESD 36

RESULT 2
US-09-770-528-8
Sequence 8, Application US/0970528
Patent No. US20020164332A1

A/Map position: 1p21-1p21
 A/Intons: 561/3, 579/3, 597/3, 615/3, 633/3, 648/3, 666/3, 681/3
 A/Note: the list of introns is incomplete
 C/Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains and one alpha 3(XI) chain (see PIR:CGH6C), initially linked by disulfide bonds among their carboxyl-
 C/Function: med with desmosine cross-links made from lysine and allysine residues
 A/Description: structural component of extracellular fibrous polymer associated with cell
 A/Note: may play a role in controlling the lateral growth of collagen II fibrils
 C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
 C/Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline
 F/1-36/Domain: signal sequence #status predicted <SIG>
 F/35-266/Domain: PARP-like #status predicted <PARP>
 F/37-511/Domain: amino-terminal propeptide #status predicted <PRO>
 F/512-1565/Produce: collagen alpha 1(XI) chain #status predicted <MAT>
 F/512-557/Region: amino-terminal nonhelical telopeptide
 F/528-1542/Region: helical
 F/1543-1565/Region: carboxyl-terminal nonhelical telopeptide
 F/1566-1806/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F/1583-1806/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
 F/61-243,112-236/Disulfide bonds: #status predicted
 F/505/Modified site: allysine (Lys) #status predicted
 F/612,1452/Modified site: 5-hydroxylysine (Lys) #status predicted
 F/612,1452/Binding site: carbohydrate (Lys) (covalent) #status predicted

Query Match 25.3%; Score 47.5; DB 1; Length 1806;
 Best Local Similarity 23.3%; Pred. No. 4,2e+02;
 Matches 14; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

QY 6 VEDNCINFAVMKPF-----DNTLYFIADDDNLESD 36
 DB 1686 VEGNSIMVQNTFKLITASARQNTYHCQSAAAYDVSSGYDKALFLGSDNDEMSYD 1745

RESULT 39
 S69031
 hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: S69031
 R/Pulten, L.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of S. cerevisiae cosmid 9659.
 A/Reference number: S69022
 A/Accession: S69031
 A/Molecule type: DNA
 A/Residues: 1-250 <FTL>
 A/Cross-references: UNIPROT:Q06511; EMBL:U40829; NID:g1066476; PID:g1066480; GSPDB:GN000
 C/Genetics:
 A/Gene: MIPS:YPR143w
 A/Cross-references: SGD:S0006347
 A/Map position: 16R

Query Match 25.0%; Score 47; DB 2; Length 250;
 Best Local Similarity 38.2%; Pred. No. 61;
 Matches 13; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 3 ABEVDNCINFAVMKPFIDNTLYFIADDDNLESD 36
 DB 48 ABEDEONSSSDSSKIIDNQSDAEDDDDEEED 81

RESULT 40
 S75062
 transcription regulator of rubisco operon - Synechocystis sp. (strain PCC 6803)
 N/Alternate names: protein sll1594
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S75062
 R/Kaneko, T.; Sato, S.; Kocant, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S75062
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-316 <KAN>
 A/Cross-references: UNIPROT:P73862; EMBL:D90910; GB:AB001339; NID:g1652956; PID:BA01792
 C/Genetics:
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 A/Gene: rbcR
 C/Superfamily: transcription activator LysR-type

Query Match 25.0%; Score 47; DB 2; Length 316;
 Best Local Similarity 36.4%; Pred. No. 78;
 Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MAEPEVDNCINFAVMKPFIDNTLYFIADDDNLESD 33
 DB 146 IVSEPEEIDLNLY--QPFIDNPLVIVARRDHPL 176

Search completed: May 13, 2005, 12:25:56
 Job time : 40 secs

submitted to the EMBL Data Library, November 1995

A>Description: The sequence of C. elegans comid C18B2.

A.Reference number: Z18368

A.Accession: J15551

A.Status: preliminary/ translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-673 <STE>

A.Cross-references: UNIPROT:O18076; EMBL:U0413; NID:g1065467; PID:g1065470; PIDN:AAA814

C/Genetics:

A.Gene: CESP:C18B2.5

A.Introns: 31/3; 101/3; 182/3; 214/1; 269/3; 372/1; 399/3; 474/2; 528/3; 640/3

C.Superfamily: Caenorhabditis elegans hypothetical protein C18B2.5

Query Match 25.3%; Score 47.5; DB 2; Length 673;

Best Local Similarity 27.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 8; Mismatches 10; Indels 19; Gaps 2;

Qy 3 AEPVNDNCINPV-----AMKFIINTYFIAEDDENLESD 36

Db 91 ATPVNDLNVSAVTLPVNLHGHDALHLEALY--GEDHSTVSE 139

RESULT 35

528791

collagen alpha 1(XI) chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S28791

R/NaH. H.D. Barenbaum, M.; Upholt, W.B.

J. Biol. Chem. 267, 22581-22586, 1992

A>Title: The chicken alpha1(XI) collagen gene is widely expressed in embryonic tissues.

A.Reference number: S28791; MUID:93054557; PMID:1429607

A.Accession: S28791

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-888 <NA>

A.Cross-references: UNIPROT:Q90796; EMBL:M88593; NID:g211619; PIDN:AAA48707.1; PID:g2116

C.Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology

F/665-887/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 25.3%; Score 47.5; DB 2; Length 888;

Best Local Similarity 23.3%; Pred. No. 2e+02;

Matches 14; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

Qy 6 VEDNCINPVAMKFI-----DNTLYFIADDEENLESD 36

Db 768 VEGNINNVQMTFLKLASARQNTYCHQSVAMHDASSDYDAKATFLGSDHEMAYD 827

RESULT 36

554697

DNA polymerase III - Mycoplasma pulmonis

C/Species: Mycoplasma pulmonis

C/Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S54697; S49397

R/Barnes, M.H.; Tarranto Jr., P.M.; Spaccapoli, P.; Brown, N.C.; Yu, H.; Dybvig, K.

Mol. Microbiol. 13, 843-854, 1994

A>Title: DNA polymerase III of Mycoplasma pulmonis: isolation and characterization of th

A.Reference number: S54697; MUID:95115554; PMID:781943

A.Accession: S54697

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-1435 <BAR>

A.Cross-references: UNIPROT:P47729; EMBL:U06833; NID:g487435; PIDN:AAA18178.1; PID:g4874

R/Dybvig, K.; Yu, H.

Mol. Microbiol. 12, 547-560, 1994

A>Title: Regulation of a restriction and modification system via DNA inversion in Mycopl

A.Reference number: S49391; MUID:95020589; PMID:7934878

A.Accession: S49397

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1408-1435 <DYB>

A.Cross-references: GB:L25415; NID:g496153; PIDN:AAA55635.1; PID:g496160

C/Genetics:

A.Genetic code: SGC3

C.Superfamily: DNA-directed DNA polymerase III alpha chain polC

Query Match 25.3%; Score 47.5; DB 2; Length 1435;

Best Local Similarity 48.0%; Pred. No. 3.3e+02;

Matches 12; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 12 NFVAMKFIINTLYF--IAEDDENL 33

Db 495 NFLKQKFIENNIFREEMISIDTLNL 519

RESULT 37

C90596

hypothetical protein MYPV 6750 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: C90596

R/Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulr

A.Reference number: A99512; MUID:21267165; PMID:11353084

A.Accession: C90596

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-1435 <CUR>

A.Cross-references: UNIPROT:P47729; GB:A1445566; PID:g14090090; PIDN:CAC13848.1; GSPDB:C

A.Experimental source: strain UAB CTIP

C/Genetics:

A.Gene: MYPV 6750

A.Genetic code: SGC3

C.Superfamily: DNA-directed DNA polymerase III alpha chain polC

Query Match 25.3%; Score 47.5; DB 2; Length 1435;

Best Local Similarity 48.0%; Pred. No. 3.3e+02;

Matches 12; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 12 NFVAMKFIINTLYF--IAEDDENL 33

Db 495 NFLKQKFIENNIFREEMISIDTLNL 519

RESULT 38

C9HUL6

collagen alpha 1(XI) chain precursor - human

N/Alternate names: procollagen alpha 1(XI) chain

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 08-May-1998

C/Accession: A35239; A31795

R/Yoshioaka, H.; Ramirez, F.

J. Biol. Chem. 265, 6423-6426, 1990

A>Title: Pro-alpha1(XI) collagen. Structure of the amino-terminal propeptide and express

A.Reference number: A35239; MUID:9020924; PMID:1690726

A.Accession: A35239

A.Molecule type: mRNA

A.Residues: 1-558 <YOS>

A.Cross-references: GB:J05407

R/Bernard, M.; Yoshioaka, H.; Rodriguez, E.; van der Rest, M.; Kimura, T.; Ninomiya, Y.;

J. Biol. Chem. 263, 17159-17166, 1988

A>Title: Cloning and sequencing of pro-alpha1(XI) collagen cDNA demonstrates that type X

cartilaginous tissue.

A.Reference number: A92689; MUID:89034222; PMID:3182841

A.Accession: A31795

A.Molecule type: DNA; mRNA

A.Residues: 538-1806 <BER>

A.Cross-references: GB:J04177

A>Note: parts of this sequence were determined by protein sequencing

C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (

ed and subsequently O-glycosylated.

C/Genetics:

A.Gene: GDB:CO11A1; COL16

A.Cross-references: GDB:120595; OMIM:120280

Query Match 25.5%; Score 48; DB 2; Length 480;
 Best Local Similarity 33.7%; Pred. No. 89;
 Matches 10; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

4 EPEVNCINFAVAMKFIIDNTLYFIADDE 31
 DB 73 EKIDELONFEGMKRKNKNDLYSLVQSD 100

RESULT 30

A:3688

hypotheical protein BH0305 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: A83688

R/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83688; MUID:20515582; PMID:11058132

A/Accession: A83688

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-284 <STO>

A/Cross-references: UNIPROT:Q9K310; GB:A001508; GB:BA000004; NID:g10172890; PIDN:BA040

C/Genetics:

A/Experimental source: strain C-125

C/Accession: BH0305

Query Match 25.3%; Score 47.5; DB 2; Length 284;
 Best Local Similarity 33.3%; Pred. No. 60;
 Matches 12; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

2 AAEPEVNCINFAVAMKFIIDNTLYFIADDE 34
 DB 87 AIOAKENNRFTIYTSIANKQDPFIADHRETE 122

RESULT 31
 T19937
 hypotheical protein C44H4.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T19937

R/Title: R.

submitted to the EMBL Data Library, August 1996

A/Reference number: Z19200

A/Accession: T19937

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-367 <WIL>

A/Cross-references: UNIPROT:Q9J372; EMBL:Z79598; PIDN:CAB01863.1; GSPDB:GN00028; CESP:C4

A/Experimental source: clone C44H4

C/Genetics:

A/Accession: CESP:C44H4.6

A/Map position: X

A/Intons: 41/3; 75/3; 100/3; 216/1; 248/3; 280/3

C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 25.3%; Score 47.5; DB 2; Length 367;
 Best Local Similarity 32.3%; Pred. No. 78;
 Matches 10; Conservative 10; Mismatches 6; Indels 5; Gaps 2;

7 EDNCINFAVAMKFIIDNTLYFIADDE 33
 DB 101 QERCLNFV-MEFMPCOLAYVHRQFAHDKOM 130

RESULT 32

B31795

collagen alpha 1(XI) chain - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: B31795
 R/Bernard, M.; Yoshioka, H.; Rodriguez, B.; van der Reest, M.; Kimura, T.; Ninomiya, Y.;
 J. Biol. Chem. 263, 17159-17166, 1988

A/Title: Cloning and sequencing of pro-alpha(XI) collagen cDNA demonstrates that type 2

cartilaginous tissue

A/Reference number: A92689; MUID:89034222; PMID:3182841

A/Accession: B31795

A/Molecule type: mRNA

A/Residues: 1-482 <BER>

A/Cross-references: UNIPROT:P20909

C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology

C/Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix

F1259-481/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 25.3%; Score 47.5; DB 2; Length 482;
 Best Local Similarity 23.3%; Pred. No. 1e+02;
 Matches 14; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

6 VEDNCINFAVAMKFIIDNTLYFIADDE 36
 DB 362 VEGNSIMVQMTFLKLTSSARQNFYNGHSTAWYDVLSGSYDKLRFSGNDEMSYD 421

RESULT 33
 T02539
 hypotheical protein At2g37730 [imported] - Arabidopsis thaliana

N/Alternate names: hypotheical protein F13M22.23

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C/Accession: T02539; D84796

R/Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, June 1998

A/Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.

A/Reference number: Z14677

A/Accession: T02539

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-532 <RCU>

A/Cross-references: UNIPROT:O80941; EMBL:AC004684; NID:g1236234; PID:g1236255

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.B.; Umayam, L.; Tallon, L.

euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: D84796

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-532 <STO>

A/Cross-references: GB:A002093; NID:g1236255; PIDN:AAC23643.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

A/Intons: 165/2; 295/3; 478/3

C/Superfamily: Arabidopsis hypotheical protein F13M22.23

Query Match 25.3%; Score 47.5; DB 2; Length 532;
 Best Local Similarity 37.9%; Pred. No. 1.2e+02;
 Matches 11; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

8 DNCINFAVAMKFIIDNTLYFIADDE 36
 DB 204 DNLIT-VLANKYDHQNTYIGNSSEVED 231

RESULT 34

T15551

hypotheical protein C18B2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15551

R/Stellies, L.

RESULT 26

S71376

glutamate receptor homolog - cherry salmon

C/Species: Oncorhynchus masou (cherry salmon)

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C/Accession: S71376

R/Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.

F/BS: Letc. 392, 71-76, 1996

A/Title: Cloning and characterization of a bifunctional metabotropic receptor activated

A/Reference number: S71376; PMID:8769318

A/Accession: S71376

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1218 <KUB>

A/Cross-References: UNIPROT:Q902F3

C/Keywords: glycoprotein; phosphoprotein

F/603-623/Domain: transmembrane #status predicted <TM1>

F/640-660/Domain: transmembrane #status predicted <TM2>

F/672-690/Domain: transmembrane #status predicted <TM3>

F/717-737/Domain: transmembrane #status predicted <TM4>

F/761-783/Domain: transmembrane #status predicted <TM5>

F/796-817/Domain: transmembrane #status predicted <TM6>

F/826-850/Domain: transmembrane #status predicted <TM7>

F/104-233/403-525/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/636-699/961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre

F/705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F/892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic

Query Match

Best Local Similarity 25.8%; Score 48.5; DB 2; Length 1218;

Matches 11; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

DB 953 NAMEFSDLSKTLNVAEDES 974

Qy 14 VAMKPTDNTLYFAEDDEN 32

S71376

laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C/Accession: S28399; S18253

R/Kusche-Gulberg, M.; Garrisson, K.; Mackrell, A.J.; Fessler, L.I.; Fessler, J.H.

EMBO J. 11, 4519-4527, 1992

A/Title: Laminin A chain: expression during Drosophila development and genomic sequence.

A/Reference number: S28399; PMID:93049203; PMID:1425586

A/Accession: S28399

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-3712 <KUS>

A/Cross-References: UNIPROT:O00174; GB:M96388; NID:g157799; PIDN:AAA2662.1; PID:g157800

R/Garrison, K.; Mackrell, A.J.; Fessler, J.H.

U. Biol. Chem. 266, 22899-22904, 1991

A/Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct

A/Reference number: S18253; PMID:92078147; PMID:1744083

A/Accession: S18253

A/Molecule type: mRNA

A/Residues: 1762-3712 <GAR>

A/Cross-References: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798

C/Genetics:

A/Gene: FLYBase:lanA

C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

F/273-330/Domain: laminin-type EGF-like homology <LEG>

F/333-400/Domain: laminin-type EGF-like homology <LEG2>

F/541-584/Domain: laminin-type EGF-like homology <LEG3>

F/176-215/Domain: III <DOM3>

F/176-186/Domain: laminin-type EGF-like homology #status atypical <LE1>

F/1809-1866/Domain: laminin-type EGF-like homology <LE2>

F/1859-1914/Domain: laminin-type EGF-like homology <LE3>

F/1917-1967/Domain: laminin-type EGF-like homology <LE4>

F/1970-2014/Domain: laminin-type EGF-like homology <LE5>

F/2017-2061/Domain: laminin-type EGF-like homology <LE6>

F/2064-2109/Domain: laminin-type EGF-like homology <LE7>

F/2116-2697/Domain: laminin-type EGF-like homology <LE7>

F/2116-2697/Domain: laminin-type EGF-like homology <LE7>

F/2698-2863/Domain: G <DOM4>

F/2698-2863/Domain: repeat G1 <RG1>

F/2864-3048/Domain: repeat G2 <RG2>

F/3048-3223/Domain: repeat G3 <RG3>

F/3079-3300/Domain: laminin G repeat homology <LG3>

F/3334-3528/Domain: repeat G4 <RG4>

F/3529-3712/Domain: repeat G5 <RG5>

F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

Query Match

Best Local Similarity 25.8%; Score 48.5; DB 2; Length 3712;

Matches 9; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

DB 3580 SYALIELVDNTLYFTVKTDKNIVS 3604

Qy 12 NFVAMKPTDNTLYFAEDDEN 35

S71376

hypothetical protein orf209 (imported) - Guillardia theta nucleomorph

C/Species: nucleomorph Guillardia theta

A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: H90128

R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei

Nature 410, 1091-1096, 2001

A/Title: The highly reduced genome of an enslaved algal nucleus.

A/Reference number: A99082; PMID:11323671; PMID:11323671

A/Accession: H90128

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-209 <DOU>

A/Cross-References: UNIPROT:Q98659; GB:AF083031; NID:g13794346; PIDN:AAK9723.1; GSPDB:G

C/Genetics:

A/Gene: orf209

A/Map position: 3

A/Genome: nucleomorph

C/Keywords: nucleomorph

Query Match

Best Local Similarity 25.5%; Score 48; DB 2; Length 209;

Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

DB 85 NFIIINSIIKSFPIEDDGNIE 107

Qy 12 NFVAMKPTDNTLYFAEDDEN 34

S71376

hypothetical protein C17G10.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T34102

R/Johnson, D.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of C. elegans cosmid C17G10.

A/Reference number: Z21476

A/Accession: T34102

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-480 <JOH>

A/Cross-References: UNIPROT:O09973; EMBL:U28739; PIDN:AAK93451.1; GSPDB:GN00020; CESP:CI

A/Experimental source: strain Bristol N2; clone C17G10

C/Genetics:

A/Gene: CESP:C17G10.1

A/Map position: 2

A/Introns: 51/1, 116/2, 158/3, 191/1, 299/3, 430/3

A/Map position: 1L

Query Match 26.1% Score 49; DB 2; Length 1628;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 21 NTLFYIADDDNLES 35
 |||||

DB 303 NLOIYKEDDENLES 317

RESULT 22

T09308

Immediate-early protein - human herpesvirus 6 (strain UI102)

C/Species: human herpesvirus 6
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T09308
 R/Nicholas, J.; Martin, M.

J. Virol. 68, 597-610, 1994

A/Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu

A/Reference number: Z16644; MUID:94118404; PMID:8289364

A/Accession: T09308
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-285 <NTC>

A/Cross-references: UNIPROT:Q89432; EMBL:L25528; NID:9451932; PIDN:AAA16721.1; PID:94519

C/Genetics: B1F2
 A/Superfamily: human herpesvirus 6 transcription regulator B701

Query Match 25.8% Score 48.5; DB 2; Length 285;
 Best Local Similarity 28.2%; Pred. No. 44;
 Matches 11; Conservative 5; Mismatches 12; Indels 11; Gaps 1;

QY 4 EPVEDNCI-----NFVAKFIDNTLYFIADDE 31
 |||||

DB 49 EETRDVCLTKTIVFAGDEKFGDLPVNETIYLAETTE 87

RESULT 23

JC4374

sterol uptake protein 1 - Yeast (Saccharomyces cerevisiae)

N/Alternate names: protein G1828; Protein YGL162w; SUT1 protein

C/Species: Saccharomyces cerevisiae
 C/Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C/Accession: JC4374; S60424; S64178
 R/Bourc, S.; Karet, F.

Gene 165, 97-102, 1995
 A/Title: Isolation and characterization of the Saccharomyces cerevisiae SUT1 gene involv

A/Reference number: JC4374; MUID:96084960; PMID:7489925

A/Accession: JC4374
 A/Molecule type: DNA

A/Residues: 1-299 <BOU>
 A/Cross-references: UNIPROT:P53032; EMBL:X77766; NID:9183994; PIDN:CAAS4806.1; PID:9118

A/Experimental source: SBI
 R/Tames, C.M.; Indge, K.J.; Oliver, S.G.

Yeast 11, 1433-1439, 1995
 A/Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromos

A/Reference number: S60417; MUID:96158061; PMID:8585324

A/Accession: S60424
 A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
 A/Residues: 1-299 <JAM>

A/Cross-references: EMBL:Z48618
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

R/Tames, C.M.; Indge, K.J.; Oliver, S.G.
 submitted to the Protein Sequence Database, May 1996

A/Reference number: S64165
 A/Accession: S64178

A/Molecule type: DNA
 A/Residues: 1-299 <JAM>
 A/Cross-references: EMBL:Z72684; NID:91322757; PID:9243599; PID:91322758; MIPS:YGL162w
 A/Experimental source: strain S288C

C/Comment: This protein is a member of the hypoxic gene family, and is rich in serine an

C/Genetics: SGD:SUT1

A/Species: SGD:S0003130; MIPS:YGL162w

A/Map position: 7L
 C/Superfamily: Saccharomyces cerevisiae hypothetical protein YPR009w

F/13-151/Region: serine/threonine-rich

Query Match 25.8% Score 48.5; DB 2; Length 299;
 Best Local Similarity 33.3%; Pred. No. 46;
 Matches 13; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

QY 5 PVBDNC-----INF--VAKFIDNTLYFIADDE 30
 |||||

DB 255 PKDKCTFSKGFTRADINISSKSLKFKDTIYDIDD 293

RESULT 24

F81354

DNA/pantothenate metabolism flavoprotein Cj0822 (imported) - Campylobacter jejuni (stra

C/Species: Campylobacter jejuni
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: F81354
 R/Parthill, J.; Wren, B.W.; Mungall, K.; Kerley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barr

Nature 403, 665-668, 2000
 A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A/Reference number: A81250; MUID:20150912; PMID:10688204

A/Accession: F81354
 A/Status: preliminary

A/Molecule type: DNA
 A/Residues: 1-384 <PAR>

A/Cross-references: UNIPROT:Q9PPA1; GB:AL139076; GB:AL111168; NID:96968128; PIDN:CAB7308

A/Experimental source: serotype O2, strain NCTC 11168
 C/Genetics:

A/Genes: dfr; Cj0822
 C/Superfamily: pantothenate metabolism flavoprotein dfr

Query Match 25.8% Score 48.5; DB 2; Length 384;
 Best Local Similarity 30.0%; Pred. No. 60;
 Matches 12; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 2 AAEPVDNCINFVAKFID-----NTLYFIADDDN 32
 |||||

DB 324 AKSLDKDKLDWVCLNIDQKVFSGDQWELVYITLNNEN 363

RESULT 25

WZVZG1

glt protein - Amasacta moorei poxvirus

C/Species: Amasacta moorei poxvirus
 C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C/Accession: A41561
 R/Hall, R.L.; Meyer, R.W.

J. Virol. 65, 6516-6527, 1991
 A/Title: Identification, cloning, and sequencing of a fragment of Amasacta moorei entomop

A/Reference number: A41561; MUID:92046310; PMID:1942245

A/Accession: A41561
 A/Molecule type: DNA

A/Residues: 1-464 <HAL>
 A/Cross-references: UNIPROT:P29817; GB:W71782; NID:9209631; PIDN:AAA42379.1; PID:9209632

C/Superfamily: vaccinia virus I7 protein
 C/Keywords: late protein

Query Match 25.8% Score 48.5; DB 1; Length 464;
 Best Local Similarity 57.9%; Pred. No. 73;
 Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAKF---IDNTLYFI 26
 |||||

DB 20 INFMSLFFSKIDNMVYFI 38

Db 147 AKTANDSINFSAADITLTL 170

RESULT 17

VPXR4S

outer layer protein VP3 - simian rotavirus SA11 (fragment)

CISpecies: simian rotavirus SA11

A/Note: host (monkey)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A04129

R/ Lopez, S.; Arias, C.F.; Bell, J.R.; Strauss, J.H.; Espajo, R.T.

Virology 144, 11-19, 1985

A/Title: Primary structure of the cleavage site associated with trypsin enhancement of

A/Reference number: A04129; MUID:86045932; PMID:2998038

A/Accession: A04129

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: genomic RNA

A/Residues: 1-747 <TOP>

A/Cross-references: UNIPROT:P04508; GB:M1158; NID:961868

C/Genetic8:

A/Map position: segment 4

C/Supfamily: rotavirus outer layer protein VP3

Query Match 26.1%; Score 49; DB 1; Length 747;
Best Local Similarity 52.6%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLFIADDDENLES 35
663 KPIPNRAYVIRKDEVLEA 681

RESULT 18

VEXR83

outer layer protein VP3 - bovine rotavirus A (strain C486)

N/Alternate names: hemagglutinin

C/Species: bovine rotavirus A

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: A29529

R/ Porter, A.A.; Cox, G.; Parker, M.; Babiuk, L.A.

Nucleic Acids Res. 15, 4361, 1987

A/Title: The complete nucleotide sequence of bovine rotavirus C486 gene 4 cDNA.

A/Reference number: A29529; MUID:87231020; PMID:3035492

A/Accession: A29529

A/Molecule type: genomic RNA

A/Residues: 1-776 <TOP>

A/Cross-references: GB:Y00127; NID:961854; PIDN:CAA68325.1; PID:961855

C/Genetic8:

A/Map position: segment 4

C/Supfamily: rotavirus outer layer protein VP3

Query Match 26.1%; Score 49; DB 1; Length 776;
Best Local Similarity 52.6%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLFIADDDENLES 35
666 KPIPNRAYVIRKDEVLEA 684

RESULT 19

VEXR81

outer layer protein VP3 - simian rotavirus SA11 (strain SA11-FEM)

N/Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3

C/Species: simian rotavirus SA11

A/Note: host (monkey)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: B31159

R/Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan

J. Virol. 62, 4022-4026, 1988
A/Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si

A/Reference number: A94694; MUID:89012172; PMID:2845121

A/Accession: B31159

A/Molecule type: genomic RNA

A/Residues: 1-776 <NIS>

A/Cross-references: UNIPROT:P17463

C/Genetic8:

A/Map position: segment 4

C/Supfamily: rotavirus outer layer protein VP3

C/Keywords: glycoprotein; hemagglutinin; outer capsid protein

P/1-241/Product: outer layer protein VP3 #status predicted <VP3>

P/248-776/Product: outer layer protein VP5 #status predicted <VP5>

P/32,56,97,132,151,198,456,507,602/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match

26.1%; Score 49; DB 1; Length 776;
Best Local Similarity 52.6%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLFIADDDENLES 35
666 KPIPNRAYVIRKDEVLEA 684

RESULT 20

S24410

hypothetical outer capsid protein - simian rotavirus SA11

C/Species: simian rotavirus SA11

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S24410

R/Mattion, N.M.; Bates, M.K.

Arch. Virol. 120, 109-113, 1991

A/Title: Sequence of a rotavirus gene 4 associated with unique biologic properties.

A/Reference number: S24410; MUID:92028406; PMID:1656916

A/Accession: S24410

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-776 <MAT>

A/Cross-references: UNIPROT:Q96802; UNIPROT:Q71293; EMBL:X57319

C/Supfamily: rotavirus outer layer protein VP3

Query Match

26.1%; Score 49; DB 2; Length 776;
Best Local Similarity 52.6%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLFIADDDENLES 35
666 KPIPNRAYVIRKDEVLEA 684

RESULT 21

T38055

hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T38055; T38177; S62429

R/Liye, G.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1995

A/Reference number: Z21765

A/Accession: T38055

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-26 <LY1>

A/Cross-references: UNIPROT:009779; EMBL:569219; PIDN:CAA93223.1; GSPDB:GN00066; SPDB:SP

R/Liye, G.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, October 1995

A/Reference number: Z21776

A/Accession: T38177

A/Molecule type: DNA

A/Residues: 8-1621 <LY2>

A/Cross-references: EMBL:Z54285; NID:91008429; PIDN:CAA91079.2; GSPDB:GN00066; SPDB:SPAC

C/Genetic8:

A/Map position: SPAC1D4.14

RESULT 12
AE2254
hypothetical protein alx588 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Notes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AE2254
R/Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriuchika, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Ref. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AE2254
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-908 <KUR>
A/Cross-references: UNIPROT:Q8Y6Z; GB:BA000019; PIDD:BAF5287.1; PID:G17132721; GSPDB:C
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alx588

Query Match 26.6%; Score 50; DB 2; Length 908;
Best Local Similarity 72.7%; Pred. No. 92;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 19 IDNTLYFIAD 29
DB 795 VDNLTLYEVAND 805

RESULT 13
T16604
hypothetical protein K10B2.5 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16604
R/Miller, N.
Submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid K10B2.
A/Reference number: 218545
A/Accession: T16604
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1109 <MIL>
A/Cross-references: UNIPROT:Q09994; EMBL:U28730; NID:G860694; PID:G860699; PIDD:AA68262
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CSDP:K10B2.5
A/Introns: 29/3; 126/1; 175/2; 226/2; 266/1; 328/2; 389/2; 527/3; 732/1; 790/3; 982/2

Query Match 26.3%; Score 49.5; DB 2; Length 1009;
Best Local Similarity 37.5%; Pred. No. 1.2e+02;
Matches 12; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 3 AEPVEDNCINFAVAKFIDNTLYFIADDDNTLE 34
DB 109 SEPMQDNKEKVVTNFIIDSM---IEDHREYE 137

RESULT 14
E97088
beta-xyloridase, family 43 glycosyl hydrolase CAC1529 [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: E97088
R/Kolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: E97088

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <KUR>
A/Cross-references: UNIPROT:Q971W1; GB:AE001437; PIDD:AAK79496.1; PID:G15024478; GSPDB:C
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Gene: CAC1529
C/Superfamily: Streptomycetes chartreusis alpha-L-arabinofuranosidase II

Query Match 26.1%; Score 49; DB 2; Length 327;
Best Local Similarity 32.6%; Pred. No. 43;
Matches 15; Conservative 6; Mismatches 13; Indels 12; Gaps 2;

QY 3 AEPVE-----DNCINFAVAKFIDNT--LYFIADDDNTLESD 36
DB 53 AEPVDVWRHRESGEMSNLTMAPRHHINAGWYTFAPADKNIEDD 98

RESULT 15
A82890
hypothetical protein U9451 [imported] - *Ureaplasma urealyticum*
C/Species: *Ureaplasma urealyticum*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: A82890
R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Caswell, G.H.
Submitted to Genbank, February 2000
A/Description: The complete sequence of *Ureaplasma urealyticum*. Alternate views of a min
A/Reference number: A82870
A/Accession: A82890
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-338 <GLA>
A/Cross-references: GB:AE002141; GB:AF222894; NID:G6899434; PIDD:AAF30863.1; GSPDB:GN001
A/Experimental source: serovar 3; biovar 1
C/Genetics:
A/Gene: U9451
A/Genetic code: GCG3

Query Match 26.1%; Score 49; DB 2; Length 338;
Best Local Similarity 32.4%; Pred. No. 44;
Matches 11; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 3 AEPVEDNCINFAVAKFIDNTLYFIADDDNTLESD 36
DB 225 AQLVYDECLAPQSSVFNNRYFIEBYRHIDP 258

RESULT 16
H96911
uroporphyrinogen III synthase [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: H96911
R/Kolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: H96911
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-490 <KUR>
A/Cross-references: UNIPROT:Q97WU3; GB:AE001437; PIDD:AAK78083.1; PID:G15022922; GSPDB:G
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Gene: CAC0098
C/Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III sy

Query Match 26.1%; Score 49; DB 2; Length 490;
Best Local Similarity 45.8%; Pred. No. 66;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 3 AEPVEDNCINFAVAKFIDNTLYFI 26

Db 600 EKIDLRCSYISINIKIHIHYKXMDNLFYTTTDDENISS 840

RESULT 3

hypothetical protein F31A3.5 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: 129700

R/Murray, J., Le, T.T.

A/Description: The sequence of *C. elegans* cosmid F31A3.

A/Reference number: 22067

A/Accession: 129700

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-780 <MOR>

A/Cross-references: UNIPROT:P09057, EMBL:U58742, PDB:1AAB36859.1, GSPDB:GN00028, CESP:F3

A/Experimental source: strain Bristol N2; clone F31A3

C/Genetics:

A/Map position: X

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

Query Match

Best Local Similarity 29.8%; Score 56; DB 2; Length 780;

Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 49 PVEDNCINFMKFIIDNTLYFIADDENL 34

RESULT 4

889961

hypothetical protein SA1584 [imported] - *Staphylococcus aureus* (strain N315)

C/Species: *Staphylococcus aureus*

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 12-Jul-2004

C/Accession: G89961

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Chii, L.; Oguchi, A.; Mizutani-Ue, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

A/Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A/Reference number: A89758; MUID:11311952; PMID:11418146

A/Accession: G89961

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-275 <KOR>

A/Cross-references: UNIPROT:Q997A3, GB:BA000018; PID:913701559; PDB:1BAB2852.1; GSPDB:C

A/Experimental source: strain N315

C/Genetics:

A/Map position: X

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Staphylococcus aureus*

A/Map position: X

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Staphylococcus aureus*

R/Bussey, H.; Keng, T.; Storme, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac

A/Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the 5

A/Reference number: 553485

A/Accession: 553485

A/Molecule type: DNA

A/Residues: 1-687 <BUS>

A/Cross-references: UNIPROT:P80235, EMBL:L28920, NID:G1616966; PID:AA09495.1; PID:9456

A/Experimental source: strain W.

A/Title: The ethanol-inducible YAT1 gene from yeast encodes a presumptive mitochondrial

A/Reference number: 547902; MUID:94086564; PMID:8262985

A/Accession: 547902

A/Molecule type: DNA

A/Residues: 1-24, 'T', 26-392, 'S', 393-594, 'AS', 597-652, 'T', 654-659, 'A', 661-687 <SCH>

A/Cross-references: EMBL:X74553, NID:G3937542; PID:CA52647.1; PID:G3937543

A/Note: the authors translated the codon GCT for residue 596 as Ser and TCG for residue

C/Genetics:

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

A/Initons: 48/2, 137/2, 188/3, 261/3, 312/2, 370/3, 452/2, 486/3, 593/1, 615/2, 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

A/Map position: 1R

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 12:16:10 / Search time 38 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188
Sequence: 1 MAEPVEDNCINFAVAKRFIDNTLYPIADNDENLESD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0
Maximum Match 100%

Listing first 45 summaries

Database: EIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	58.5	192	2	S60226
2	62.5	33.2	1398	2	H71606
3	56	29.8	780	2	T29700
4	55	29.3	275	2	G89961
5	55	29.3	687	2	S53485
6	53	28.2	365	2	B81307
7	52.5	27.9	212	2	G97866
8	52	27.7	736	2	T00023
9	51	27.1	647	2	T28214
10	50	26.6	302	2	T38789
11	50	26.6	536	2	A56590
12	50	26.6	908	2	AE2254
13	49.5	26.3	1009	2	T16604
14	49	26.1	327	2	E97088
15	49	26.1	338	2	A82890
16	49	26.1	490	2	H56911
17	49	26.1	747	1	VPKRS43
18	49	26.1	776	1	VPKRS43
19	49	26.1	776	1	VPKRS43
20	49	26.1	776	1	VPKRS43
21	49	26.1	1628	2	T38055
22	48.5	25.8	285	2	T09308
23	48.5	25.8	299	2	JC4374
24	48.5	25.8	384	2	F81354
25	48.5	25.8	464	1	MZVZG1
26	48.5	25.8	1318	2	S71376
27	48.5	25.8	3712	2	S18253
28	48	25.5	209	2	H90128
29	48	25.5	480	2	T34102

30	47.5	25.3	284	2	A83688	hypothetical prote
31	47.5	25.3	367	2	T19337	hypothetical prote
32	47.5	25.3	482	2	B31795	collagen alpha 1(X
33	47.5	25.3	532	2	T02539	hypothetical prote
34	47.5	25.3	673	2	T15551	hypothetical prote
35	47.5	25.3	888	2	S28791	collagen alpha 1(X
36	47.5	25.3	1435	2	S54637	DNA polymerase III
37	47.5	25.3	1435	2	C90596	hypothetical prote
38	47.5	25.3	1806	1	CGHUIE	collagen alpha 1(X
39	47.5	25.0	250	2	S69031	hypothetical prote
40	47	25.0	316	2	S75062	transcription regu
41	47	25.0	357	2	T38405	hypothetical prote
42	47	25.0	443	1	A0CLOA	glutamate-ammonia
43	47	25.0	468	2	B72351	cholesterol-relate
44	47	25.0	502	2	T29729	hypothetical prote
45	47	25.0	571	2	S68356	pept protein - Sta

ALIGNMENTS

RESULT 1
S60226
Cytokine IGIF - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60226
R/Okamura, H., Teutscher, H., Komatsu, T., Yutsudo, M., Hakura, A., Tanimoto, T., Torigoe, Nature 378, 88-91, 1995
A/Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A/Reference number: S60226; MUID:96061009; PMID:7477296
A/Accession: S60226
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-192 <OK>
A/Cross-references: UNIPROT:P70380; EMBL:D49949; NID:G1064822; PIDD:BA08705.1; PID:G106
C/Superfamily: Mus musculus cytokine IGIF

Query Match 58.5% Score 110; DB 2; Length 192;
Best Local Similarity 66.7% Pred. No. 9.1e-08;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFAVAKRFIDNTLYPIADNDENLESD 36
DB 6 EDSCVFKEMKFIIDNTLYPIADNDENLESD 35

RESULT 2

H71606
Hypothetical protein PF80755w - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: H71606
R/Gardner, M.J., Tetteh, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Patter, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O. Science 282, 1126-1133, 1998
A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Accession: H71606
A/Molecule type: DNA
A/Residues: 1-1398 <GAR>
A/Cross-references: UNIPROT:O96244; GB:AE001416; GB:AE001362; NID:G3845268; PIDD:AACT194
A/Experimental source: clone 3D7
A/Genes: PF80755w

Query Match 33.2% Score 62.5; DB 2; Length 1398;
Best Local Similarity 31.7% Pred. No. 2.7;
Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 4 EPVEDNCINFAVAKRFIDNTLYPIADNDENLESD 35

FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36
DB 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36

RESULT 5

US-08-832-180-9
Sequence 9, Application US/08832180
Patent No. 6214584

GENERAL INFORMATION:

APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKUTSU
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakui
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Netmark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:

APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 100.0%; Score 188; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36
DB 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36

RESULT 6

US-10-105-080-4
Sequence 4, Application US/10105080
Patent No. 6806479

GENERAL INFORMATION:

APPLICANT: SAMYANG GENEX CORPORATION
APPLICANT: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
TITLE OF INVENTION: GENE THERAPY USING THEM
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopatentlin 1.71
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Human interleukin-18 precursor mutant
US-10-105-080-4

Query Match 100.0%; Score 188; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36
DB 1 MAAPEVDNCINFAMKFIINTLYFLAEDDENLESD 36

RESULT 7

US-09-949-016-6095
Sequence 6095, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

APPLICATION NUMBER: 60/237,768
FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

SOFTWARE: FastSeq for Windows Version 4.0

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6095
LENGTH: 193
TYPE: PRT
ORGANISM: Human
US-09-949-016-6095

Query Match 100.0%; Score 188; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;

Matches 36, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
QY 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36
DB 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36

RESULT 8

US-09-597-576-2
Sequence 2, Application US/09597576
Patent No. 6432678
GENERAL INFORMATION:
APPLICANT: Alexander Taylor
APPLICANT: Han Trinh
TITLE OF INVENTION: MACACA CYNOMOLGUS IL18
FILE REFERENCE: GP-70629
CURRENT APPLICATION NUMBER: US/09/597,576
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/140,140
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

Query Match
Best Local Similarity 95.2%; Score 179; DB 4; Length 193;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36
DB 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36

RESULT 9

US-09-917-265A-2
Sequence 2, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 133
TYPE: PRT
ORGANISM: Felis catus
FEATURE:
NAME/KEY: m18c.feature
LOCATION: (119)..(119)
OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
US-09-917-265A-2

Query Match
Best Local Similarity 74.2%; Score 139.5; DB 4; Length 133;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36
DB 1 MTAIPVDD-CINFGMKFIIDNTLYFAEDDENSED 35

RESULT 10

US-09-917-265A-8
Sequence 8, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 192
TYPE: PRT
ORGANISM: Felis catus
US-09-917-265A-8

Query Match
Best Local Similarity 74.2%; Score 139.5; DB 4; Length 192;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36
DB 1 MTAIPVDD-CINFGMKFIIDNTLYFAEDDENSED 35

RESULT 11

US-09-445-724B-2
Sequence 2, Application US/09445724B
Patent No. 6600020
GENERAL INFORMATION:
APPLICANT: OKANO, FUMIYOSHI
TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
TITLE OF INVENTION: ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
TITLE OF INVENTION: PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
FILE REFERENCE: 2109-15
CURRENT APPLICATION NUMBER: US/09/445,724B
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Caninus sp.
US-09-445-724B-2

Query Match
Best Local Similarity 70.2%; Score 132; DB 4; Length 193;
Matches 25; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFAEDDENSED 36
DB 1 MATNIEDNCINLVAMKFNNTLYFKASDEGLESD 36

RESULT 12

US-09-445-724B-6
Sequence 6, Application US/09445724B
Patent No. 6600020
GENERAL INFORMATION:
APPLICANT: OKANO, FUMIYOSHI
TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
TITLE OF INVENTION: ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
TITLE OF INVENTION: PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
FILE REFERENCE: 2109-15
CURRENT APPLICATION NUMBER: US/09/445,724B
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1

ORGANISM: Chironomus tentans

US-09-564-418-9

Query Match 26.6%; Score 50; DB 4; Length 536;
 Best Local Similarity 38.5%; Pred. No. 36;
 Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 11 INFVAMKFDINTLYFIADENLESD 36
 DB 16 INVASQSFQNNIYGATKKORLESD 41

RESULT 17

US-09-107-532A-6689
 ; Sequence 6689, Application US/09107532A
 ; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arindello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6689:

SEQUENCE CHARACTERISTICS:

LENGTH: 569 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...569

SEQUENCE DESCRIPTION: SEQ ID NO: 6689:

US-09-107-532A-6689

Query Match 26.3%; Score 49.5; DB 4; Length 569;
 Best Local Similarity 45.2%; Pred. No. 47;
 Matches 14; Conservative 4; Mismatches 8; Indels 5; Gaps 2;QY 8 DNCINFVAM--KFDINTLYFIADENLESD 36
 DB 71 DNPENFVAMLRKYLQGA---IIEIDIEQIEND 98RESULT 18
 US-09-248-796A-27329

Sequence 27329, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keth Weinlock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 27329

LENGTH: 78

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-27329

Query Match 26.1%; Score 49; DB 4; Length 78;
 Best Local Similarity 33.3%; Pred. No. 5;
 Matches 10; Conservative 8; Mismatches 12; Indels 0; Gaps 0;QY 5 PVEDNCINFVAMKFDINTLYFIADENLE 34
 DB 29 PVENNFFFGSSHINTQIYLSINESVE 58RESULT 19
 US-09-134-000C-6071
 ; Sequence 6071, Application US/09134000C
 ; Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6071

LENGTH: 367

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-6071

Query Match 26.1%; Score 49; DB 4; Length 367;
 Best Local Similarity 31.0%; Pred. No. 33;
 Matches 9; Conservative 8; Mismatches 12; Indels 0; Gaps 0;QY 4 EPVEDNCINFVAMKFDINTLYFIADEN 32
 DB 180 QEIKVNDVVVALFAFDRTALITSDPEN 208RESULT 20
 US-08-089-397A-16
 ; Sequence 16, Application US/08089397A
 ; Patent No. 6086880

GENERAL INFORMATION:

APPLICANT: SABA, MARTA I.T.

APPLICANT: FRENCHICK, PATRICK J.

APPLICANT: POTTER, ANDREW A.

APPLICANT: IJAZ, MOHAMMAD K.

APPLICANT: GILCHRIST, JAMES E.

APPLICANT: REDMOND, MARK J.

TITLE OF INVENTION: ROTAVIRUS VACCINES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSES: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,397A
FILING DATE: 07-JUL-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 29311-20003.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-089-397A-16

Query Match 26.1% Score 49; DB 3; Length 747;
Best Local Similarity 52.6%; Pred. No. 77;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0.

17 KFIIDNTLYFIADDDNTLS 35
Db 663 KFIIDNTLYFIADDDNTLS 681

RESULT 21
US-07-603-1338-17
Sequence 17, Application US/076031338
Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,1338
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250

```

; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: AMINO ACID
; STRADEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-603-1338-17

Query Match 25.1%; Score 49; DB 1; Length 776;
Bee Local Similarity 52.6%; Pred. No. 81;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 17 KEIDNTLYFIAEDDENIES 35
||| ||| ||| ||| |||
Db 666 KEIPNRAVYAKDDDEVLDA 684

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      RESULT 22  

      US-07-603-133B-20  

      ; Sequence 20 Application US/07603133B  

      ; Patent No. 5298244  

      ; GENERAL INFORMATION:  

      APPLICANT: Redmond, Mark J.  

      APPLICANT: Ijaz, Mohammed K.  

      APPLICANT: Parker, Michael D.  

      TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR  

      TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE  

      NUMBER OF SEQUENCES: 30  

      CORRESPONDENCE ADDRESS:  

      ADDRESSEE: Morrison & Foerster  

      STREET: 545 Middlefield Road, Suite 200  

      CITY: Menlo Park  

      STATE: CA  

      COUNTRY: USA  

      ZIP: 94025  

      COMPUTER READABLE FORM:  

      MEDIUM TYPE: Floppy disk  

      COMPUTER: IBM PC compatible  

      OPERATING SYSTEM: PC-DOS/MS-DOS  

      SOFTWARE: Patentin Release #1.0, Version #1.25  

      CURRENT APPLICATION DATA:  

      APPLICATION NUMBER: US/07/603.133B  

      FILING DATE: 19901025  

      CLASSIFICATION: 42A  

      ATTORNEY/AGENT INFORMATION:  

      NAME: Robins, Roberta L.  

      REGISTRATION NUMBER: 33,208  

      REFERENCE/DOCKET NUMBER: 9313-0004.00  

      TELECOMMUNICATION INFORMATION:  

      TELEPHONE: (415) 327-7250  

      TELEFAX: (415) 327-2951  

      TELEX: 7061141  

      INFORMATION FOR SEQ ID NO: 20:  

      SEQUENCE CHARACTERISTICS:  

      LENGTH: 776 amino acids  

      TYPE: AMINO ACID  

      TOPOLOGY: linear  

      MOLECULE TYPE: protein  

      US-07-603-133B-20  

      Query Match 26.1%; Score 49; DB 1; Length 776;  

      Best Local Similarity 52.6%; Pred. No. 81;  

      Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  

      17 KEIDENTIFYPARENTHESIS 35  

      ||| | :||| :  

      666 KFLPNRAVRYIKODEVLEA 684
    
```

RESULT 23

US-08-089-397A-15
 / Sequence 15, Application US/08089397A
 / Patent No. 6086880
 / GENERAL INFORMATION:
 / APPLICANT: SABAR, MARTA I. J.
 / APPLICANT: FRENCHICK, PATRICK J.
 / APPLICANT: POTTER, ANDREW A.
 / APPLICANT: IJAZ, MOHAMMAD K.
 / APPLICANT: GILCHRIST, JAMES B.
 / APPLICANT: REDMOND, MARK J.
 / TITLE OF INVENTION: ROTAVIRUS VACCINES
 / NUMBER OF SEQUENCES: 24
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: MORRISON & FORSTER
 / STREET: 2000 Pennsylvania Avenue, NW
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20006-1888
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/089,397A
 / FILING DATE: 07-JUL-1993
 / CLASSIFICATION: 530
 / ATTORNEY/AGENT INFORMATION:
 / NAME: ADLER, REID G.
 / REGISTRATION NUMBER: 30,988
 / REFERENCE/DOCKET NUMBER: 29311-20003.03
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202) 887-1500
 / TELEFAX: (202) 887-0763
 / INFORMATION FOR SEQ ID NO: 15:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 776 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: unknown
 / TOPOLOGY: unknown
 / MOLECULAR TYPE: protein
 / US-08-089-397A-15

Query Match 26.1%; Score 49; DB 3; Length 776;
 Best Local Similarity 52.6%; Pred. No. 81;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KPIDNTLYPIADNDNTLES 35
 DB 666 KPIDNRAVVIDEVLTA 684

RESULT 24
 US-07-991-867B-2
 / Sequence 2, Application US/07991867B
 / Patent No. 5476781
 / GENERAL INFORMATION:
 / APPLICANT: MOYER, Richard W.
 / APPLICANT: Hall, Richard L.
 / APPLICANT: Gruidl, Michael E.
 / TITLE OF INVENTION: No. 5476781 Entomopoxvirus Expression System
 / NUMBER OF SEQUENCES: 66
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David R. Saliwanchik
 / STREET: 2421 N.W. 41st Street, Suite A-1
 / CITY: Gainesville
 / STATE: FL
 / COUNTRY: USA
 / ZIP: 32606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/991,867B
 / FILING DATE: 19-FEB-1991
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / PRIOR APPLICATION NUMBER: US 07/827,658
 / FILING DATE: 30-JAN-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/657,584
 / FILING DATE: 19-FEB-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Saliwanchik, David R.
 / REGISTRATION NUMBER: 31,794
 / REFERENCE/DOCKET NUMBER: UP114.C3
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 904-375-8100
 / TELEFAX: 904-372-5800
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 464 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULAR TYPE: protein
 / US-07-991-867B-2

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/991,867B
 FILING DATE: 12-DEC-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 92/14818
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,685
 FILING DATE: 30-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,584
 FILING DATE: 19-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: UP114.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-07-991-867B-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
 Best Local Similarity 57.9%; Pred. No. 51;
 Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKE---IDNTLYPI 26
 DB 20 INFMSMLPFSSKIDNNVYPI 38

RESULT 25
 US-08-107-755A-2
 / Sequence 2, Application US/08107755A
 / Patent No. 5721352
 / GENERAL INFORMATION:
 / APPLICANT: MOYER, Richard W.
 / APPLICANT: Hall, Richard L.
 / APPLICANT: Gruidl, Michael E.
 / TITLE OF INVENTION: No. 5721352 Entomopoxvirus Expression System
 / NUMBER OF SEQUENCES: 40
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David R. Saliwanchik
 / STREET: 2421 N.W. 41st Street, Suite A-1
 / CITY: Gainesville
 / STATE: Florida
 / COUNTRY: U.S.A.
 / ZIP: 32606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/107,755A
 / FILING DATE: 19-AUG-1993
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / PRIOR APPLICATION NUMBER: US 07/827,658
 / FILING DATE: 30-JAN-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/657,584
 / FILING DATE: 19-FEB-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP14.C2
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-755A-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
DB 20 INFMSMLFPSKIDNMYFI 38

RESULT 26
US-08-544-332-2
Sequence 2, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael B.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION/DOCKET NUMBER: 35,746
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-544-332-2

Query Match 25.8%; Score 48.5; DB 2; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
DB 20 INFMSMLFPSKIDNMYFI 38

RESULT 27
US-09-370-861A-2
Sequence 2, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael B.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UP14.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Amasacta moorei entomopoxvirus
US-09-370-861A-2

Query Match 25.8%; Score 48.5; DB 4; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
DB 20 INFMSMLFPSKIDNMYFI 38

RESULT 28
US-09-134-000C-6731
Sequence 6731, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6731
LENGTH: 93
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6731

Query Match 25.5%; Score 48; DB 4; Length 93;
 Best Local Similarity 42.3%; Pred. No. 8.8;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAARVEDNCINFMVAKPFDNTLYPI 26
 DB 16 MLSPDENILISFVGIVFIDNLYLLI 41

RESULT 29
 US-09-248-796A-20803
 Sequence 20803, Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 PRIOR FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 20803
 LENGTH: 520
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-20803

Query Match 25.5%; Score 48; DB 4; Length 520;
 Best Local Similarity 47.1%; Pred. No. 70;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 20 DNTLYFIADDEDESD 36
 DB 44 DNVLYFIKENEGIIIDPD 60

RESULT 30
 US-09-113-750A-3
 Sequence 3, Application US/09113750A
 Patent No. 6294176

GENERAL INFORMATION:
 APPLICANT: David E. Junker and Mark D. Cochran
 TITLE OF INVENTION: Recombinant Raccoonpox virus
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113,750A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 55744
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 262-0400
 TELEFAX: (212) 664-0525
 TELEX: 422523

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 688 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-113-750A-3

Query Match 25.5%; Score 48; DB 3; Length 688;
 Best Local Similarity 43.5%; Pred. No. 98;
 Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 7 EDNCINFMVAKPFDNTLYPIAD 29
 DB 222 EQICINLVKKYPLDINVINFIROD 244

RESULT 31
 US-09-328-352-5474
 Sequence 5474, Application US/09328352
 Patent No. 6562958

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 5474
 LENGTH: 1039
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-5474

Query Match 25.3%; Score 47.5; DB 4; Length 1039;
 Best Local Similarity 25.6%; Pred. No. 1.9e+02;
 Matches 11; Conservative 9; Mismatches 10; Indels 13; Gaps 1;

QY 5 EVENCINFMVAKPFDNT-----LYFIADDEDESD 34
 DB 568 PKEDGILSVQIKVDSPISQSIGQVQYFLIQEDKAVD 610

RESULT 32
 US-09-919-497-56
 Sequence 56, Application US/09919497
 Patent No. 6773883

GENERAL INFORMATION:
 APPLICANT: Muller, George L.
 TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 FILE REFERENCE: B0801/7225
 CURRENT APPLICATION NUMBER: US/09/919,497
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/221,735
 PRIOR FILING DATE: 2000-07-31
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 56
 LENGTH: 1806
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: UNSURE
 LOCATION: (758)..(758)
 OTHER INFORMATION: Xaa = any amino acid
 NAME/KEY: UNSURE
 LOCATION: (809)..(809)
 OTHER INFORMATION: Xaa = any amino acid
 US-09-919-497-56

Query Match 25.3%; Score 47.5; DB 4; Length 1806;
Best Local Similarity 23.3%; Pred. No. 3.8e+02;
Matches 11; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

QY 6 VEDNCINFAVAMKFTI-----DNTYFIAEDDENTESD 36
DB 1686 VEGSINMVMQMTFLKLTASARQNTFYHCHQSAAWYDVSSQSYKALRFLGSDNEBMSYD 1745

RESULT 33
US-09-212-247C-4
Sequence 4, Application US/09212247C
Patent No. 6391603

GENERAL INFORMATION:

APPLICANT: POMEYUS, Markus, SUELBARGER, Harald, JOEFFKEN, Hans
Wolfgang, DOVAL, Jose Luis Revuelta, JIMENEZ, Alberto;
and GARCIA, Maria Angeles Santos
TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Goseypil
and the use thereof in microbial riboflavin
synthesis

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kell & Weinkauff

STREET: 1101 Connecticut Avenue

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: IBM AT-compatible, Pentium processor

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect version 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/212,247C

FILING DATE: 16-Dec-1998

CLASSIFICATION: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-212-247C-4

Query Match 25.0%; Score 47; DB 3; Length 475;
Best Local Similarity 43.5%; Pred. No. 89;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAEVEDNCINFAVAMKFTIDNTLY 24
DB 77 AASVALDSLINFVAVKYFNNEKY 99

RESULT 34
US-09-746-359A-39

Sequence 39, Application US/09746359A

Patent No. 6610286

GENERAL INFORMATION:

APPLICANT: Thompson, Penny

APPLICANT: Foster, Donald C.

APPLICANT: Xu, Wenfeng

APPLICANT: Madden, Karen L.

APPLICANT: Kelly, James D.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Blumberg, Hal

APPLICANT: Eagan, Maribeth A.

APPLICANT: Jaspers, Stephen R.

APPLICANT: Chandrasekhar, Yasmin A.

APPLICANT: No. 6610286ak, Julia E.

TITLE OF INVENTION: Method for Treating Inflammation

FILE REFERENCE: 99-108

CURRENT APPLICATION NUMBER: US/09/746,359A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/171,969

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/213,341

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 39

LENGTH: 514

TYPE: PRT

ORGANISM: Mus musculus

US-09-746-359A-39

Query Match 25.0%; Score 47; DB 4; Length 514;
Best Local Similarity 36.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 4 EPEVEDNCINFAVAMKFTIDNTLYFIAEDDENTL 33
DB 273 EPEITITLNFITFSMLDTRK--ISPRDNTL 300

RESULT 35

US-09-746-359A-37

Sequence 37, Application US/09746359A

Patent No. 6610286

GENERAL INFORMATION:

APPLICANT: Thompson, Penny

APPLICANT: Foster, Donald C.

APPLICANT: Xu, Wenfeng

APPLICANT: Madden, Karen L.

APPLICANT: Kelly, James D.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Blumberg, Hal

APPLICANT: Eagan, Maribeth A.

APPLICANT: Jaspers, Stephen R.

APPLICANT: Chandrasekhar, Yasmin A.

APPLICANT: No. 6610286ak, Julia E.

TITLE OF INVENTION: Method for Treating Inflammation

FILE REFERENCE: 99-108

CURRENT APPLICATION NUMBER: US/09/746,359A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/171,969

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/213,341

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 37

LENGTH: 546

TYPE: PRT

ORGANISM: Mus musculus

US-09-746-359A-37

Query Match 25.0%; Score 47; DB 4; Length 546;
Best Local Similarity 36.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 4 EPEVEDNCINFAVAMKFTIDNTLYFIAEDDENTL 33
DB 305 EPEITITLNFITFSMLDTRK--ISPRDNTL 332

RESULT 36

US-08-895-522-4

Sequence 4, Application US/08895522

Patent No. 5858719

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
TITLE OF INVENTION: TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,522
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0336 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 575393
US-08-895-522-4

Query Match 25.0%; Score 47; DB 2; Length 694;
Best Local Similarity 43.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 2 AAEVPEVNCINFVAKKEIDNTLY 24
Db 298 AASVALDSLINFBAVKYFNNEKY 320

RESULT 37
US-09-195-391-4
Sequence 4, Application US/09195391
Patent No. 6080842
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
TITLE OF INVENTION: TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,391
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0336 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 575393
US-09-195-391-4

Query Match 25.0%; Score 47; DB 3; Length 694;
Best Local Similarity 43.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 2 AAEVPEVNCINFVAKKEIDNTLY 24
Db 298 AASVALDSLINFBAVKYFNNEKY 320

RESULT 38
US-07-603-133B-15
Sequence 15, Application US/07603133B
Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohamed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSES: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids

TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-133B-15

Query Match 25.0%; Score 47; DB 1; Length 775;
Best Local Similarity 45.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 17 KFIIDNTLYFIADDDNLESD 36
DB 665 KFIPIKRAYRVLKDDDEVMEAD 684

RESULT 39
US-07-603-133B-16
Sequence 16, Application US/07603133B
Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-133B-16

Query Match 25.0%; Score 47; DB 1; Length 775;
Best Local Similarity 45.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 17 KFIIDNTLYFIADDDNLESD 36
DB 665 KFIPIKRAYRVLKDDDEVMEAD 684

RESULT 40
US-09-538-092-323
Sequence 323, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:

APPLICANT: Gluc, Lotc
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurataseqFormatter Version 0.9
SEQ ID NO 323
LENGTH: 818
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YGI229C
US-09-538-092-323

Query Match 24.7%; Score 46.5; DB 4; Length 818;
Best Local Similarity 25.5%; Pred. No. 2e+02;
Matches 13; Conservative 8; Mismatches 15; Indels 15; Gaps 2;

QY 1 MAAPVEDNDCIN-----FVAMKFIIDNTLYFIAB-DDENLESD 36
DB 498 ITSNLTLEDKNNNSNDNSNDNOKKXKXKGFHNEIYSTFDSDDNIDD 548

Search completed: May 13, 2005, 12:26:43
Job time : 43 secs